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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:02:07 ; Search time 16.5871 Seconds
(without alignments)
3219.466 Million cell updates/sec

Title: US-09-830-972-29_COPY_990_1178
Perfect score: 931
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	931	100.0	893	3	AAY95012	Aay95012 Human sec
2	931	100.0	983	6	ABU11573	Abu11573 Human MDD
3	931	100.0	1178	3	AAY71311	Aay71311 Human neu
4	931	100.0	1192	3	AAY56967	Aay56967 Human MAG
5	931	100.0	1192	4	AAB82349	Aab82349 Human NOG
6	931	100.0	1192	4	AAU04591	Aau04591 Human Nog
7	931	100.0	1192	5	ABG30938	Abg30938 Human Nog
8	931	100.0	1192	5	ABP68600	Abp68600 Human pan
9	931	100.0	1192	5	ABB81078	Abb81078 Human neu

10	931	100.0	1192	6	ABR59667	Abr59667	Human	Nog
11	928	99.7	200	4	AAB64514	Aab64514	Human	sec
12	927	99.6	199	2	AAW53947	Aaw53947	Human	NSP
13	927	99.6	199	2	AAW78313	Aaw78313	Fragment	
14	927	99.6	199	3	AAB12805	Aab12805	Human	NSP
15	927	99.6	199	4	AAB82348	Aab82348	Human	NOG
16	927	99.6	199	5	ABB81080	Abb81080	Human	neu
17	927	99.6	373	3	AAAY53624	Aay53624	A bone	ma
18	927	99.6	373	3	AAAY56969	Aay56969	Human	MAG
19	927	99.6	373	3	AAB24242	Aab24242	Human	Nog
20	927	99.6	373	4	AAB82350	Aab82350	Human	NOG
21	927	99.6	373	5	AAM47954	Aam47954	Human	RTN
22	927	99.6	373	5	ABG30937	Abg30937	Human	Nog
23	927	99.6	373	5	ABP68601	Abp68601	Human	pan
24	927	99.6	373	5	ABB81079	Abb81079	Human	neu
25	923	99.1	291	4	AAM93484	Aam93484	Human	pol
26	918	98.6	199	2	AAAY35903	Aay35903	Extended	
27	908	97.5	361	3	AAAY71385	Aay71385	Alternati	
28	908	97.5	1163	3	AAAY71310	Aay71310	Rat	neuri
29	908	97.5	1163	3	AAAY71384	Aay71384	Alternati	
30	908	97.5	1163	5	ABB81074	Abb81074	Rat	neuro
31	906	97.3	199	3	AAAY71559	Aay71559	Rat	Nogo
32	906	97.3	359	3	AAAY71558	Aay71558	Rat	Nogo
33	906	97.3	403	3	AAAY71563	Aay71563	Rat	Nogo
34	906	97.3	1162	3	AAAY71557	Aay71557	Rat	Nogo
35	905	97.2	379	7	ADB85283	Adb85283	Rat	fooce
36	904	97.1	199	5	ABB81077	Abb81077	Rat	neuro
37	904	97.1	360	3	AAAY71383	Aay71383	Rat	neuri
38	904	97.1	360	5	ABB81076	Abb81076	Rat	neuro
39	904	97.1	522	3	AAAY71312	Aay71312	Rat	neuri
40	894.5	96.1	642	2	AAW58383	Aaw58383	Human	sec
41	894.5	96.1	642	4	AAB90682	Aab90682	Human	BG1
42	886	95.2	199	5	ABG30939	Abg30939	Human	Nog
43	851	91.4	175	2	AAW78194	Aaw78194	Human	sec
44	682	73.3	202	4	AAB64513	Aab64513	Gene 27	h
45	682	73.3	208	3	AAB12808	Aab12808	NSPC	prot

ALIGNMENTS

RESULT 1

AAAY95012

ID AAY95012 standard; protein; 893 AA.

XX

AC AAY95012;

XX

DT 19-JUN-2000 (first entry)

XX

DE Human secreted protein vb22_1, SEQ ID NO:64.

XX

KW Human; secreted protein; cancer; tumour; cardiovascular disorder;

KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;

KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;

KW neurodegenerative disease; asthma; contraceptive.

XX

OS Homo sapiens.

XX
 PN WO200011015-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 24-AUG-1999; 99WO-US019351.
 XX
 PR 24-AUG-1998; 98US-0097638P.
 PR 24-AUG-1998; 98US-0097659P.
 PR 09-SEP-1998; 98US-0099618P.
 PR 28-SEP-1998; 98US-0102092P.
 PR 25-NOV-1998; 98US-0109978P.
 PR 23-DEC-1998; 98US-0113645P.
 PR 23-DEC-1998; 98US-0113646P.
 PR 23-AUG-1999; 99US-00379246.
 XX
 PA (ALPH-) ALPHAGENE INC.
 XX
 PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
 XX
 DR WPI; 2000-224657/19.
 XX
 PT New secreted or transmembrane proteins and polynucleotides encoding them,
 PT useful for treating neurodegenerative disorders, autoimmune diseases and
 PT cancer.
 XX
 PS Claim 73; Page 322-325; 357pp; English.
 XX
 CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
 CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins
 CC of the invention include those that are thought to be only partially
 CC secreted, i.e., transmembrane proteins. The proteins of the invention may
 CC exhibit one or more activities selected from the following: cytokine
 CC activity; cell proliferation; differentiation; immune modulation;
 CC haematopoiesis regulation; tissue growth activity; activin/inhibin
 CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic
 CC activity; anti-inflammatory activity; and tumour inhibition activity. The
 CC proteins may be administered to patients as vaccines, and the nucleotides
 CC may be used as part of a gene therapy regime. Diseases or conditions that
 CC may be treated using the proteins or nucleotides of the invention include
 CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular
 CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;
 CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;
 CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and
 CC allergic reactions such as asthma and anaemia. They may also be used for
 CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal
 CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease
 CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin
 CC activity may additionally be useful as contraceptives. Nucleic acid
 CC sequences of the invention may be used in chromosome mapping, and as a
 CC source of diagnostic primers and probes. The present sequence represents
 CC one of the 40 proteins of the invention
 XX
 SQ Sequence 893 AA;

Query Match 100.0%; Score 931; DB 3; Length 893;
 Best Local Similarity 100.0%; Pred. No. 4.4e-92;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      705 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 764

Qy      61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLQFAV 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      765 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLQFAV 824

Qy      121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      825 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 884

Qy      181 IPGLKRKAE 189
        ||||||||
Db      885 IPGLKRKAE 893
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RESULT 2

ABU11573

ID ABU11573 standard; protein; 983 AA.

XX

AC ABU11573;

XX

DT 12-FEB-2003 (first entry)

XX

DE Human MDDT polypeptide SEQ ID 520.

XX

KW MDDT; human; disease detection and treatment molecule polypeptide;
KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW gene therapy; protein replacement therapy; cell proliferative disorder;
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
KW psoriasis; hepatitis.

XX

OS Homo sapiens.

XX

PN WO200279449-A2.

XX

PD 10-OCT-2002.

XX

PF 27-MAR-2002; 2002WO-US009944.

XX

PR 28-MAR-2001; 2001US-0279619P.

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.

PR 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.

PR 20-JUN-2001; 2001US-0299776P.

PR 20-JUN-2001; 2001US-0300001P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX
 DR WPI; 2003-058431/05.
 DR N-PSDB; ABX34563.
 XX
 PT New purified disease detection and treatment molecule proteins and
 PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis.
 XX
 PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.
 XX
 CC This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are
 CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
 CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
 CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 983 AA;

Query Match 100.0%; Score 931; DB 6; Length 983;
 Best Local Similarity 100.0%; Pred. No. 5e-92;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 795 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQA 854
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 855 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 914
 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 915 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 974
 Qy 181 IPGLKRKAE 189
 ||||||||
 Db 975 IPGLKRKAE 983

RESULT 3

AAY71311

ID AAY71311 standard; protein; 1178 AA.

XX

AC AAY71311;

XX

DT 02-NOV-2000 (first entry)

XX

DE Human neurite growth inhibitor Nogo.

XX

KW Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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FT	Misc-difference	187
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	188
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	189
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	190
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	221
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	328
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	477
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Region	977. .1012
----	--------	------------

FT		/note= "Region specifically described in claim 16"
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FT	Region	994. .1174
----	--------	------------

FT		/note= "Region specifically described in claim 16"
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FT	Region	1079. .1114
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FT		/note= "Region specifically described in claim 16"
----	--	--

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US026160.

XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 11; Fig 13; 122pp; English.
XX
CC The present sequence is a human Nogo protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. The human Nogo
CC sequence was derived by aligning human expressed sequence tags (ESTs)
CC e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092565, AA081525
CC and AA081840 with the rat Nogo sequence. Nogo proteins and fragments
CC displaying neurite growth inhibitory activity are used in the treatment
CC of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However the specification does not include sequences for
CC these SEQ ID numbers
XX
SQ Sequence 1178 AA;

Query Match 100.0%; Score 931; DB 3; Length 1178;
Best Local Similarity 100.0%; Pred. No. 6.4e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 60
|
Db 990 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 1049
Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
|
Db 1050 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1109
Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
|
Db 1110 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1169
Qy 181 IPGLKRKAE 189
|
Db 1170 IPGLKRKAE 1178

RESULT 4
AA56967
ID AA56967 standard; protein; 1192 AA.

XX
 AC AAY56967;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human MAGI polypeptide.
 XX
 KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;
 KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
 KW psychiatric disorder; developmental disorder; inflammatory disorder;
 KW stroke; cytostatic; cerebroprotective; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 PN WO200005364-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-GB002360.
 XX
 PR 22-JUL-1998; 98GB-00016024.
 PR 19-JUL-1999; 99GB-00016898.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Michalovich D, Prinjha RK;
 XX
 DR WPI; 2000-182693/16.
 DR N-PSDB; AAZ56886.
 XX
 PT Novel polypeptides related to neuroendocrine-specific proteins and
 PT polynucleotides useful for diagnosis of various diseases and for
 PT treatment of cancer and neurological disorders.
 XX
 PS Claim 2; Page 20-21; 35pp; English.
 XX
 CC The invention relates to human MAGI protein, which is similar to
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
 CC and antibodies are useful for treating diseases, including neuropathies,
 CC spinal injury, neuronal degeneration, neuromuscular disorders,
 CC psychiatric disorders and developmental disorders, cancer, stroke and
 CC inflammatory disorders. The polynucleotide is also useful for chromosome
 CC localization and for tissue expression studies. The present sequence
 CC represents the human MAGI protein
 XX
 SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 3; Length 1192;
 Best Local Similarity 100.0%; Pred. No. 6.5e-92;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFAGSLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1004 SVVDLLYWRDIKKTGVVFAGSLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1063
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120

Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123
 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
 Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183
 Qy 181 IPGLKRKAE 189
 Db 1184 IPGLKRKAE 1192

RESULT 5

AAB82349

ID AAB82349 standard; protein; 1192 AA.

XX

AC AAB82349;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human NOGO-A protein.

XX

KW NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;
 KW cerebroprotective; neuroleptic; diagnosis; therapy.

XX

OS Homo sapiens.

XX

PN WO200136631-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-GB004345.

XX

PR 15-NOV-1999; 99GB-00026995.

PR 24-JAN-2000; 2000GB-00001550.

XX

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Michalovich D, Prinjha R;

XX

DR WPI; 2001-343822/36.

DR N-PSDB; AAF90324.

XX

PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
 PT gene and may be useful in the treatment of neural disorders including
 PT Alzheimer's and Parkinson's diseases.

XX

PS Disclosure; Page 26-27; 25pp; English.

XX

CC The present sequence is that of human NOGO-A. NOGO-A is a previously
 CC known splice variant of the human NOGO gene on chromosome 2p21. The
 CC invention relates to a novel splice variant, NOGO-C (see AAB82348). It
 CC provides NOGO-C polypeptides and polynucleotides, and methods for
 CC producing such polypeptides by recombinant techniques. Also disclosed are

CC methods for utilising NOGO-C polypeptides and polynucleotides in the
CC treatment of diseases including neuropathies, spinal injury, brain
CC injury, stroke, neuronal degeneration, for example Alzheimer's disease
CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders
CC and developmental disorders. Also provided are methods for identifying
CC agonists and agonists for use in treating conditions associated with NOGO
CC -C imbalance, and diagnostic assays for detecting diseases associated
CC with inappropriate NOGO-C activity or levels

XX

SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 4; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.5e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 60
|
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 1063

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
|
Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123

Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
|
Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy 181 IPGLKRKAE 189
|
Db 1184 IPGLKRKAE 1192

RESULT 6

AAU04591

ID AAU04591 standard; protein; 1192 AA.

XX

AC AAU04591;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;
KW cranial trauma; cerebral trauma; spinal cord injury; stroke;
KW demyelinating disease; multiple sclerosis; monophasis demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;
KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;
KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;
KW Canavan's disease; metachromatic leukodystrophy; viral infection;
KW Krabbe's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1054. .1119

FT /label= Lumenal_extracellular_domain

FT /note= "This sequence is specifically claimed"

FT Peptide 1055. .1094
 FT /label= Pep1
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1064. .1088
 FT /label= Pep2
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1074. .1098
 FT /label= Pep3
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1084. .1108
 FT /label= Pep4
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1095. .1119
 FT /label= Pep5
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 XX
 PN WO200151520-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001041.
 XX
 PR 12-JAN-2000; 2000US-0175707P.
 PR 26-MAY-2000; 2000US-0207366P.
 PR 29-SEP-2000; 2000US-0236378P.
 XX
 PA (UYYA) UNIV YALE.
 XX
 PI Strittmatter SM;
 XX
 DR WPI; 2001-442138/47.
 DR N-PSDB; AAS09453.
 XX
 PT Novel Nogo receptor protein useful for identifying modulator of Nogo
 PT protein or Nogo receptor protein, which is useful for treating central
 PT nervous system disorders.
 XX
 PS Example 1; Page 101-104; 109pp; English.
 XX
 CC The sequence is the human Nogo protein, a 250kDa myelin-associated axon
 CC growth inhibitor. The invention relates to the use of the nogo receptor,
 CC nogo protein, their nucleic acids, vectors expressing them and antibodies
 CC against them, to isolate agents which block nogo receptor mediated axonal
 CC growth. The agent is useful for treating a central nervous system
 CC disorder which is a result of cranial or cerebral trauma, spinal cord
 CC injury, stroke or a demyelinating disease selected from multiple
 CC sclerosis, monophasis demyelination, encephalomyelitis, multifocal
 CC leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease,
 CC pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease,
 CC Spongy degeneration, Alexander's disease, Canavan's disease,
 CC metachromatic leukodystrophy, viral infection and Krabbe's disease
 XX

SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 4; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.5e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60
          |||
Db      1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1063

Qy      61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLQKFAV 120
          |||
Db      1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLQKFAV 1123

Qy      121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
          |||
Db      1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy      181 IPGLKRKAE 189
          |||
Db      1184 IPGLKRKAE 1192
```

RESULT 7

ABG30938

ID ABG30938 standard; protein; 1192 AA.

XX

AC ABG30938;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human NogoA protein.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;
KW Nogo-associated disease; metastasis.

XX

OS Homo sapiens.

XX

PN WO200257483-A2.

XX

PD 25-JUL-2002.

XX

PF 18-JAN-2002; 2002WO-GB000228.

XX

PR 18-JAN-2001; 2001GB-00001312.

XX

PA (GLAX) GLAXO GROUP LTD.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX

DR WPI; 2002-599722/64.

DR N-PSDB; ABK90134.

AC ABP68600;
 XX
 DT 14-JAN-2003 (first entry)
 XX
 DE Human pancreatic cancer expressed protein SEQ ID NO 71.
 XX
 KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
 KW cytostatic; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200260317-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 30-JAN-2002; 2002WO-US002781.
 XX
 PR 30-JAN-2001; 2001US-0265305P.
 PR 31-JAN-2001; 2001US-0265682P.
 PR 09-FEB-2001; 2001US-0267568P.
 PR 21-MAR-2001; 2001US-0278651P.
 PR 28-APR-2001; 2001US-0287112P.
 PR 16-MAY-2001; 2001US-0291631P.
 PR 12-JUL-2001; 2001US-0305484P.
 PR 20-AUG-2001; 2001US-0313999P.
 PR 27-NOV-2001; 2001US-0333626P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
 XX
 DR WPI; 2002-627435/67.
 DR N-PSDB; ABV94680.
 XX
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic
 PT cancer.
 XX
 PS Claim 2; SEQ ID NO 71; 300pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
 CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
 CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 5; Length 1192;

Best Local Similarity 100.0%; Pred. No. 6.5e-92;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 1063

Qy      61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123

Qy      121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy      181 IPGLKRKAE 189
          ||||||||
Db      1184 IPGLKRKAE 1192
```

RESULT 9

ABB81078

ID ABB81078 standard; protein; 1192 AA.

XX

AC ABB81078;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;

KW central nervous system; peripheral nervous system; tranquillizer; Nogo;

KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;

KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;

KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;

KW neurotransmitter receptor; human; receptor.

XX

OS Homo sapiens.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;

PI Moalem G;
 XX
 DR WPI; 2002-607255/65.
 DR N-PSDB; ABN86601.
 XX
 PT Promoting nerve regeneration and preventing neuronal degeneration in the
 PT central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides.
 XX
 PS Example; Page 53-56; 93pp; English.
 XX
 CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease is
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents the human
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific
 CC antigen
 XX
 SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 5; Length 1192;
 Best Local Similarity 100.0%; Pred. No. 6.5e-92;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 1063

 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123

 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180


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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy      181 IPGLKRKAE 189
          ||||||||
Db      1184 IPGLKRKAE 1192

```

RESULT 10

ABR59667

ID ABR59667 standard; protein; 1192 AA.

XX

AC ABR59667;

XX

DT 22-JUL-2003 (first entry)

XX

DE Human NogoA protein.

XX

KW Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy;
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.

XX

OS Homo sapiens.

XX

PN WO2003031462-A2.

XX

PD 17-APR-2003.

XX

PF 04-OCT-2002; 2002WO-US032007.

XX

PR 06-OCT-2001; 2001US-00972599.

XX

PA (UYA) UNIV YALE.

XX

PI Strittmatter SM;

XX

DR WPI; 2003-393433/37.

DR

N-PSDB; ACC81048.

XX

PT New human Nogo receptor polypeptides and nucleic acids, useful for
 PT decreasing inhibition of axonal growth by a central nervous system
 PT neuron, or in treating central nervous system disease, disorder or
 PT injury, e.g. spinal cord injury.

XX

PS Disclosure; Page 131-135; 148pp; English.

XX

CC The invention relates to a novel nucleic acid encoding a polypeptide
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
 CC human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of P1 with
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS
 CC domain, provided that a partial CTS domain, if present, consists of no
 CC more than the first 39 consecutive residues. The nucleic acid of the
 CC invention has neuroprotective activity. The polynucleotide may have a use
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
 CC axonal growth by a central nervous system (CNS) neuron. The NgR.

CC polypeptide or an agent inhibits the binding of Nogo to NgR or NgR-
CC dependent signal transduction in the central nervous system neuron may be
CC used in treating central nervous system disease, disorder or injury, e.g.
CC spinal cord injury. Expression of an NgR protein may be associated with
CC inhibition of axonal regeneration following cranial, cerebral or spinal
CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
CC monophasic demyelination, encephalomyelitis, multifocal
CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
CC sequence is used in the exemplification of the invention

XX

SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 6; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.5e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60
|
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1063

Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
|
Db 1064 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123

Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
|
Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy 181 IPGLKRKAE 189
|
Db 1184 IPGLKRKAE 1192

RESULT 11

AAB64514

ID AAB64514 standard; protein; 200 AA.

XX

AC AAB64514;

XX

DT 23-MAR-2001 (first entry)

XX

DE Human secreted protein sequence encoded by gene 28 SEQ ID NO:152.

XX

KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; cerebral ischaemia; infection;
KW angiogenesis; nervous system disorder; Alzheimer's disease; skin aging;
KW ocular disorder; corneal infection; wound healing; food additive;
KW preservative.

XX

OS Homo sapiens.

XX

PN WO200077255-A1.

XX

Db 72 IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLEFLVDDLVDLSLKFAV 131

QY 121 LMWVF^TTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
 |||

Db 132 LMWVF^TTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 191

QY 181 IPGLKRKAE 189
 |||

Db 192 IPGLKRKAE 200

RESULT 12

AAW53947

ID AAW53947 standard; protein; 199 AA.

XX

AC AAW53947;

XX

DT 24-JUL-1998 (first entry)

XX

DE Human NSPLP protein A.

XX

KW NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;

KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer.

XX

OS Homo sapiens.

XX

PN WO9806841-A2.

XX

PD 19-FEB-1998.

XX

PF 24-JUL-1997; 97WO-US013469.

XX

PR 12-AUG-1996; 96US-00700607.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Bandman O, Au-Young J, Goli SK, Hillman J;

XX

DR WPI; 1998-159533/14.

DR N-PSDB; AAV23695.

XX

PT Human neuro-endocrine-specific protein-like proteins - useful for

PT diagnosis, monitoring and treatment of cancer and neuro-degenerative

PT disease.

XX

PS Claim 1; Page 38; 73pp; English.

XX

CC This sequence is a human neuroendocrine-specific protein-like protein
 CC (NSPLP) of the invention. Recombinant cells transformed with the DNA are
 CC used to express the NSPLP proteins, which are used to treat cancer and
 CC neurodegenerative diseases such as amyotrophic lateral sclerosis. Also
 CC antisense nucleic acids and antagonists of NSPLP can be used to inhibit
 CC activity of the NSPLP proteins. Antibodies specific for NSPLP are used
 CC for diagnosis and monitoring treatment of diseases associated with NSPLP
 CC expression, in usual immunoassays, and to isolate NSPLP from natural
 CC sources. The NSPLP proteins, or their fragments can also be used in drug
 CC screening to identify NSPLP antagonists. The nucleic acid can be used

PR 13-JUN-1997; 97US-0049549P.
PR 13-JUN-1997; 97US-0049550P.
PR 13-JUN-1997; 97US-0049566P.
PR 13-JUN-1997; 97US-0049606P.
PR 13-JUN-1997; 97US-0049607P.
PR 13-JUN-1997; 97US-0049608P.
PR 13-JUN-1997; 97US-0049609P.
PR 13-JUN-1997; 97US-0049610P.
PR 13-JUN-1997; 97US-0049611P.
PR 13-JUN-1997; 97US-0050901P.
PR 13-JUN-1997; 97US-0052989P.
PR 08-JUL-1997; 97US-0051919P.
PR 18-AUG-1997; 97US-0055984P.
PR 12-SEP-1997; 97US-0058665P.
PR 12-SEP-1997; 97US-0058668P.
PR 12-SEP-1997; 97US-0058669P.
PR 12-SEP-1997; 97US-0058750P.
PR 12-SEP-1997; 97US-0058971P.
PR 12-SEP-1997; 97US-0058972P.
PR 12-SEP-1997; 97US-0058975P.
PR 02-OCT-1997; 97US-0060834P.
PR 02-OCT-1997; 97US-0060841P.
PR 02-OCT-1997; 97US-0060844P.
PR 02-OCT-1997; 97US-0060865P.
PR 02-OCT-1997; 97US-0061059P.
PR 02-OCT-1997; 97US-0061060P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olsen HS;
PI Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;
PI Feng P;

XX

DR WPI; 1999-080881/07.

DR N-PSDB; AAX04379.

XX

PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.

XX

PS Disclosure; Page 62; 380pp; English.

XX

CC This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule detailed in the descriptor line. The gene
CC can be used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of
CC the fused protein as compared to the human protein only. The invention
CC relates to 86 novel genes and their fragments (nucleic acid sequences:
CC AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. Also, pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 86 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAX04311 for
CC described uses)

XX

SQ Sequence 199 AA;

Query Match 99.6%; Score 927; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.6e-92;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
          |||
Db      12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 71

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVAVL 121
          |||
Db      72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVAVL 131

Qy      122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
          |||
Db      132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy      182 PGLKRKAE 189
          |||
Db      192 PGLKRKAE 199
```

RESULT 14

AAB12805

ID AAB12805 standard; protein; 199 AA.

XX

AC AAB12805;

XX

DT 24-NOV-2000 (first entry)

XX

DE Human NSPH protein sequence SEQ ID NO:4.

XX

KW Human; neuroendocrine-specific protein; NSPH; NSPA; NSPB; NSPC.

XX

OS Homo sapiens.

XX

PN CN1253180-A.

XX

PD 17-MAY-2000.

XX

PF 30-OCT-1998; 98CN-00121473.

XX

PR 30-OCT-1998; 98CN-00121473.

XX

PA (UYFU-) UNIV FUDAN.

XX

PI Yu L, Zhao Y, Zhang H;

XX

DR WPI; 2000-466537/41.

DR N-PSDB; AAA72981.

XX

PT Specific protein of human neuroendocrine, coding sequence and its
PT preparing process and application.

XX

PS Claim 4; Page 14-15; 2lpp; Chinese.

XX

XX
DR WPI; 2001-343822/36.
DR N-PSDB; AAF90323.
XX
PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
PT gene and may be useful in the treatment of neural disorders including
PT Alzheimer's and Parkinson's diseases.
XX
PS Claim 3; Page 25; 25pp; English.
XX
CC The present sequence is that of human NOGO-C, encoded by a novel splice
CC variant of the human NOGO gene on chromosome 2p21. 2 Other splice
CC variants, NOGO-A and NOGO-B, have previously been identified. The
CC invention provides NOGO-C polypeptides and polynucleotides, and methods
CC for producing such polypeptides by recombinant techniques. Also disclosed
CC are methods for utilising NOGO-C polypeptides and polynucleotides in the
CC treatment of diseases including neuropathies, spinal injury, brain
CC injury, stroke, neuronal degeneration, for example Alzheimer's disease
CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders
CC and developmental disorders. Also provided are methods for identifying
CC agonists and agonists for use in treating conditions associated with NOGO
CC -C imbalance, and diagnostic assays for detecting diseases associated
CC with inappropriate NOGO-C activity or levels
XX
SQ Sequence 199 AA;

Query Match 99.6%; Score 927; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.6e-92;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAI	61
Db	12	VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAI	71
Qy	62	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAVL	121
Db	72	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAVL	131
Qy	122	MWVFITYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI	181
Db	132	MWVFITYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI	191
Qy	182	PGLKRKAE	189
Db	192	PGLKRKAE	199

Search completed: September 29, 2004, 18:14:01
Job time : 17.5871 secs

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:09:33 ; Search time 4.69196 Seconds
 (without alignments)
 2079.581 Million cell updates/sec

Title: US-09-830-972-29_COPY_990_1178
 Perfect score: 931
 Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	927	99.6	199	2	US-08-700-607-1	Sequence 1, Appli
2	682	73.3	208	2	US-08-700-607-7	Sequence 7, Appli
3	682	73.3	356	2	US-08-700-607-6	Sequence 6, Appli
4	682	73.3	776	2	US-08-700-607-5	Sequence 5, Appli
5	665	71.4	267	2	US-08-700-607-8	Sequence 8, Appli
6	541.5	58.2	168	4	US-09-149-476-563	Sequence 563, App
7	512	55.0	241	2	US-08-700-607-3	Sequence 3, Appli
8	285	30.6	92	4	US-09-149-476-411	Sequence 411, App
9	100	10.7	80	3	US-08-905-223-411	Sequence 411, App
10	89	9.6	468	4	US-08-487-596-8	Sequence 8, Appli
11	89	9.6	468	4	US-08-660-451A-8	Sequence 8, Appli

12	88.5	9.5	1278	4	US-09-462-136-2	Sequence 2, Appli
13	87.5	9.4	592	4	US-09-134-000C-5477	Sequence 5477, Ap
14	87.5	9.4	1051	4	US-09-134-001C-5005	Sequence 5005, Ap
15	85	9.1	414	4	US-08-956-171E-5246	Sequence 5246, Ap
16	83	8.9	744	4	US-09-785-381-1	Sequence 1, Appli
17	83	8.9	744	4	US-09-785-381-3	Sequence 3, Appli
18	82.5	8.9	554	4	US-09-252-991A-27968	Sequence 27968, A
19	81.5	8.8	598	2	US-08-853-659A-53	Sequence 53, Appl
20	81	8.7	970	4	US-09-795-927-7	Sequence 7, Appli
21	80.5	8.6	280	4	US-09-543-681A-6175	Sequence 6175, Ap
22	80.5	8.6	593	4	US-09-328-352-4866	Sequence 4866, Ap
23	79	8.5	993	4	US-08-836-687B-30	Sequence 30, Appl
24	78.5	8.4	446	4	US-09-543-681A-6579	Sequence 6579, Ap
25	78	8.4	292	4	US-09-489-039A-12212	Sequence 12212, A
26	78	8.4	349	4	US-09-198-452A-973	Sequence 973, App
27	77	8.3	154	1	US-08-366-783-5	Sequence 5, Appli
28	77	8.3	424	4	US-09-543-681A-7510	Sequence 7510, Ap
29	77	8.3	614	4	US-09-540-236-2858	Sequence 2858, Ap
30	76.5	8.2	420	4	US-09-134-001C-3805	Sequence 3805, Ap
31	76	8.2	1053	4	US-09-328-352-5058	Sequence 5058, Ap
32	75.5	8.1	397	4	US-09-328-352-7457	Sequence 7457, Ap
33	75.5	8.1	454	4	US-09-904-615-165	Sequence 165, App
34	75	8.1	248	4	US-09-198-452A-1153	Sequence 1153, Ap
35	75	8.1	1421	4	US-09-252-991A-17805	Sequence 17805, A
36	74.5	8.0	390	4	US-09-198-452A-254	Sequence 254, App
37	74	7.9	289	4	US-09-540-236-2019	Sequence 2019, Ap
38	74	7.9	1160	4	US-09-328-352-6826	Sequence 6826, Ap
39	73.5	7.9	208	4	US-09-107-532A-6378	Sequence 6378, Ap
40	73.5	7.9	517	4	US-09-540-236-2403	Sequence 2403, Ap
41	73.5	7.9	720	4	US-09-134-000C-5631	Sequence 5631, Ap
42	73	7.8	231	4	US-09-198-452A-419	Sequence 419, App
43	73	7.8	379	4	US-09-491-577-6	Sequence 6, Appli
44	73	7.8	700	4	US-09-543-681A-4969	Sequence 4969, Ap
45	72.5	7.8	408	4	US-09-107-532A-6198	Sequence 6198, Ap

ALIGNMENTS

RESULT 1

US-08-700-607-1

; Sequence 1, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

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;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette
;   COMPUTER:  IBM Compatible
;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/700,607
;   FILING DATE:  Filed Herewith
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Billings, Lucy J.
;   REGISTRATION NUMBER:  36,749
;   REFERENCE/DOCKET NUMBER:  PF-0114 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-855-0555
;   TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  .199 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   IMMEDIATE SOURCE:
;   LIBRARY:
;   CLONE:  Consensus
US-08-700-607-1

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Query Match          99.6%;  Score 927;  DB 2;  Length 199;
Best Local Similarity 100.0%;  Pred. No. 5.3e-93;
Matches 188;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 71

Qy     62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 131

Qy    122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy    182 PGLKRKAE 189
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Db    192 PGLKRKAE 199

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RESULT 2
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT:  Bandman, Olga
; APPLICANT:  Au-Young, Janice
; APPLICANT:  Goli, Surya K.
; APPLICANT:  Hillman, Jennifer L.

```

```

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311
US-08-700-607-7

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Query Match          73.3%; Score 682; DB 2; Length 208;
Best Local Similarity 68.4%; Pred. No. 2.6e-66;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

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Qy      3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 62
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Db      22 IDLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQ 81

Qy      63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLM 122
        |:|||||:|||| |: |:| :|||: :|| |:||||||| | | | | | | | | | |
Db      82 KTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLM 141

Qy      123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
        |: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      142 WLLTYVGALFNGLTLLMAVVSMTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 201

Qy      183 GLKRKAE 189
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Db      202 GAKRHAE 208

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RESULT 3
 US-08-700-607-6
 ; Sequence 6, Application US/08700607
 ; Patent No. 5858708
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,607
 ; FILING DATE: Filed Herewith
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0114 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 356 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 307309
 US-08-700-607-6

Query Match 73.3%; Score 682; DB 2; Length 356;
 Best Local Similarity 68.4%; Pred. No. 5.5e-66;
 Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

Qy 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 62
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 Db 170 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 229
 Qy 63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLM 122
 |:|||||:| | | : :|:| :| | :| | ||||| ||||| |||||
 Db 230 KTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKLRLFLVQDLVDLSLKFAVLM 289

Qy 123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
 |: ||||| |||||::|::|::|::|: ||||| |||| :: :|||
 Db 290 WLLTYVGALFNGLTLLMAVVSMTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 349

Qy 183 GLKRKAE 189
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 Db 350 GAKRHAE 356

RESULT 4

US-08-700-607-5

; Sequence 5, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 776 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 307307

US-08-700-607-5

Query Match 73.3%; Score 682; DB 2; Length 776;

Best Local Similarity 68.4%; Pred. No. 1.6e-65;

Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

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Qy	63	KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLM	122
		: : : :: : ::: : :	
Db	650	KTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLM	709
Qy	123	WVFITYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAIP	182
		: ::: ::: ::: ::: : :: :	
Db	710	WLLTYVGALFNGLTLLLMAVVSMTLPVVVVKHQAQIDQYLGLVRTHINAVVAKIQAIP	769
Qy	183	GLKRKA	189
Db	770	GAKRHAE	776

US-08-700-607-8

; Sequence 8, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

```
; STREET: 3174 Porter Drive
```

; CITY: Palo Alto

; STATE: CA

COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
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;      COMPUTER:  IBM Compatible
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;      OPERATING SYSTEM:  DOS
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; SOFTWARE: FastSEQ Version 1.5
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/700,607

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 267 amino acids

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;      TYPE:  amino acid
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; STRANDEDNESS: single
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;      MOLECULE TYPE:  peptide
;      IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  281046
US-08-700-607-8

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Query Match 71.4%; Score 665; DB 2; Length 267;
Best Local Similarity 67.2%; Pred. No. 2.6e-64;
Matches 123; Conservative 33; Mismatches 27; Indels 0; Gaps 0;

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		: :: : : : : :	
Db	13	IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ	72
Qy	63	KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDLDVDSLKFVILM	122
		: : : : : : :: : :	
Db	73	KTDEGHPFKAYLELEITLSQEIQKYTDCLQLYVNSTLKELRRLFLVQDLVDVDSLKFVILM	132
Qy	123	WVFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKIQAKIP	182
		: :: : : : : : : : :: :	
Db	133	WLLTYVGALFNGLTLLLMAVVSMTLPVVYVKHQAVDQYLGLVRTHINTVVAKIQAKIP	192
Qy	183	GLK	185
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Db	193	GAR	195

RESULT 6

US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
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; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
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; EARLIER APPLICATION NUMBER: 60/047,599
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
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; EARLIER APPLICATION NUMBER: 60/048,964
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; EARLIER APPLICATION NUMBER: 60/057,650
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; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060

; EARLIER FILING DATE: 1997-10-02

Query Match 58.2%; Score 541.5; DB 4; Length 168;
Best Local Similarity 60.5%; Pred. No. 3.7e-51;
Matches 101; Conservative 34; Mismatches 31; Indels 1; Gaps 1;

Qy 24 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEE 83
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Db 1 MLLSLAAFVISVSVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60

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Qy 144 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 189
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Db 121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKKAE 167

RESULT 7

US-08-700-607-3

; Sequence 3, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 241 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: THP1NOB01
; CLONE: 31870
US-08-700-607-3
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Query Match          55.0%; Score 512; DB 2; Length 241;
Best Local Similarity 52.4%; Pred. No. 1e-47;
Matches 98; Conservative 35; Mismatches 34; Indels 20; Gaps 1;
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RESULT 8

US-09-149-476-411

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; Sequence 411, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
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; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13

; TISSUE TYPE: Brain
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; NAME/KEY: sig_peptide
; LOCATION: -78..-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 6.3
; OTHER INFORMATION: seq TLIMLLSWQLSVS/SV
US-08-905-223-411

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Best Local Similarity 57.1%; Pred. No. 0.0015;
Matches 20; Conservative 8; Mismatches 5; Indels 2; Gaps 1;

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RESULT 10

US-08-487-596-8

; Sequence 8, Application US/08487596

; Patent No. 6440681

; GENERAL INFORMATION:

; APPLICANT: Elliot, Kathryn J.

; APPLICANT: Ellis, Steven B.

; APPLICANT: Harpold, Michael M.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND

; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL

; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,596

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO US94/02447

; FILING DATE: 08-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/149,503

; FILING DATE: 08-NOV-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/028,031

; FILING DATE: 08-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/938,154

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; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-596-8

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Query Match          9.6%; Score 89; DB 4; Length 468;
Best Local Similarity 20.9%; Pred. No. 0.28;
Matches 40; Conservative 29; Mismatches 66; Indels 56; Gaps 5;

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Db      288 VLVSLTVFLLVIEEIIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHRSSSTHNA 347

Qy      71 RAYL-----ESEVAISEELVQKYSNSALGHVNCTIKEL 103
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Db      348 MAPLVRKIFLHTLPKLLCMRSHVDTRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHI 407

Qy      104 RRLFLVDDLVDLSLK-----AVLMWVFYTVYGALFNGLTLLILALISLFSVPVIYERHQA 157
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Db      408 MKENDVREVVEDWKFIQVLDRLMFLWTFLFVS-----IVGSLGLF-VPVIYKWANI 457

Qy      158 QIDHYLGLANK 168
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Db      458 LIPVHIGNANK 468

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RESULT 11

US-08-660-451A-8

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; Sequence 8, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 06/07/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ORIGINAL SOURCE:
US-08-660-451A-8

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Query Match          9.6%; Score 89; DB 4; Length 468;
Best Local Similarity 20.9%; Pred. No. 0.28;
Matches 40; Conservative 29; Mismatches 66; Indels 56; Gaps 5;

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Qy      71 RAYL-----ESEVAISEELVQKYSNSALGHVNCTIKEL 103
      | |      |:| : : :|| : : :
Db      348 MAPLVRKIFLHTLPKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHI 407

Qy      104 RRLFLVDDLVDLSLKF-----AVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQA 157
      : | :|: || : :| | :| | : : || ||||:
Db      408 MKENDVREVVEDWKFIAQVLDRLMFLWTFLEVS-----IVGSLGLF-VPVIYKWANI 457

Qy      158 QIDHYLGLANK 168
      | :| |||
Db      458 LIPVHIGNANK 468

```

```

RESULT 12
US-09-462-136-2
; Sequence 2, Application US/09462136

```

```
; Patent No. 6426198
; GENERAL INFORMATION:
; APPLICANT: Carstea, et al.
; TITLE OF INVENTION: Genes for Niemann-Pick Type C Disease
; FILE REFERENCE: 4239-53894
; CURRENT APPLICATION NUMBER: US/09/462,136
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/US98/13862
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/051,682
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-136-2
```

```
Query Match          9.5%; Score 88.5; DB 4; Length 1278;
Best Local Similarity 25.7%; Pred. No. 1.3;
Matches 39; Conservative 25; Mismatches 51; Indels 37; Gaps 7;
```

```
Qy      46 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRR 105
      ::|||| : : : : | | | : : | : ||| || ||
Db      598 NLTISFTAERSIEDELNRESDSDF-----TVVISYAIMFLYISLALGH-----IKSCRR 647

Qy      106 LFLVDD-----LVDSLKFAVLMMWVFTYVGALFNGLTLLILALI-----SLF 146
      | ||| | : | : ||:| | ||::: | :|
Db      648 L-LVDSKVSLGIAGILIVLSSVACSLGVFSYIGL---PLTLIVIEVIPFLVLAVGVDNIF 703

Qy      147 SVPVIYERHQ----AQIDHYLGLANKNVKDAM 174
      : | : : : | || | :|
Db      704 ILVQAYQRDERLQGETLDQQLGRVLGEVAPSM 735
```

RESULT 13

```
US-09-134-000C-5477
; Sequence 5477, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5477
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5477
```

Query Match 9.4%; Score 87.5; DB 4; Length 592;
Best Local Similarity 20.8%; Pred. No. 0.56;
Matches 48; Conservative 41; Mismatches 65; Indels 77; Gaps 10;

Qy	7	YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR-----IYK	55
		: : : : : :: : : : : :	
Db	45	FWKTVKR-----LFRYMSKRMLSIIAV---LVLAIAAVVFQIQTPKVLGQATTEIFK	93
Qy	56	GVIQAIQKSDEGHPFRA-----YLESEV-----A	79
		:: : : :	
Db	94	GVMKGAEMKQGLKITSFPIDFDKIGQILLIVIAMYLISAVFNFLQQVIMTRVSQRTVYE	153
Qy	80	ISEELVQKYSNSALG----HVNCTIKELRRLFLVDDLVDLSLK---FAVLMWVFTYVGALF	132
		: : : : : : : : : : : :	
Db	154	LRQELEAKMNKVPISYYDIHSNGDIMS-RAINDMDNIASTLQQNLTLQLITSIVTFVGVWLW	212
Qy	133	NGLTL-LILALISLFSVPVIY-----ERHQAQIDHYLGLANKNVKD	172
		: : : : : :	
Db	213	MMLTISWQLTLIALATVPLSLIVVMVAVPRSQKHFAAQOKSLGLLNNOVEE	263

RESULT 14

```

US-09-134-001C-5005
; Sequence 5005, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5005
; LENGTH: 1051
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5005

```

Query Match 9.4%; Score 87.5; DB 4; Length 1051;
Best Local Similarity 22.9%; Pred. No. 1.2;
Matches 44; Conservative 35; Mismatches 68; Indels 45; Gaps 8;

Qy	2	VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSV-----TAYIALALLSVTISFRIYKG	56
		: : : : : : : ::	
Db	380	IVILLFLRNIRTTAI-----SIVSIPMSILIALIALKLSNVSLNIILTLGA	424
Qy	57	VIQAIQKSDEGHPFRAYLESEVAISEELVQKYS--NSALGHVNCTIKELRRLF---LVDD	111
		: : :: : : : : : :	
Db	425	LTVAIGR-----VIDDSIVVVENIFRRLSDPNKLGKGENLIISATREVFKEPIMSST	475
Qy	112	LVDSLKFAVLMMVFITYVGALFN---GLTLLILA--LISLFSVPVIYERHOAQIDHYLGL	165

	: :: : : :: : :	
Db	476 LVTIVVFLPLVFVSGSVGEMFRPFALAITFSLLASLLVSITLVPSLGATFFKN-----GV	530
Qy	166 ANKNVKDAMAKI	177
	: : :	
Db	531 KNREQKEGLGTV	542

RESULT 15

US-08-956-171E-5246

; Sequence 5246, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; Gil H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/956,171E

; FILING DATE: 20-Oct-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 5246:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 414 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 5246:

US-08-956-171E-5246

Query Match 9.1%; Score 85; DB 4; Length 414;
Best Local Similarity 21.8%; Pred. No. 0.63;
Matches 42; Conservative 36; Mismatches 75; Indels 40; Gaps 7;

```
Qy      2 VVDLLYWRDIKKTGV-VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQA 60
      :| ||: |:|: | : : | ||::| || | |::: : |
Db      3 IVILLFLRNIRTTAISIISIPLSLLMAL-----IALKLSDVSLNITLGLTVA 51

Qy     61 IQKSDEGHPPFRAYLESEVAISEELVQKYSNS--ALGHVNCTIKELRRLF---LVDDL VDS 115
      | : : : : | : : : : | | | | : | : ||
Db     52 IGR-----VIDDSIVVVENIYRRLTDSEEQLKGENLIISATTEVFKEPIMSSTLV TI 102

Qy    116 LKFAVLMWVFETYVGALFN-----GLTLLILALISLFSVPVI-----YERHQAQIDH 161
      : | |::| || : | : || |:: | | : : | |
Db    103 IVFLPLVFVSGSVGEMFRPFALAI AF SLLASLLVSITLVPALAAATLFKKGVKRRNKQH QE 162

Qy    162 YLGLANKNVKDAM 174
      ||: : | :
Db    163 GLGVVSTTYKKVL 175
```

Search completed: September 29, 2004, 18:21:05
Job time : 5.69196 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:05:43 ; Search time 4.62587 Seconds
(without alignments)
3930.111 Million cell updates/sec

Title: US-09-830-972-29_COPY_990_1178
Perfect score: 931
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		%				Query	Description
Result	No.	Score	Match	Length	DB	ID	
1	682	73.3	208	2	I60904	neuroendocrine-spe	
2	682	73.3	776	2	A46583	neuroendocrine-spe	
3	665	71.4	267	2	A60021	tropomyosin-relate	
4	335	36.0	2484	2	T26216	hypothetical prote	
5	335	36.0	2607	2	T26215	hypothetical prote	
6	334	35.9	222	2	T26213	hypothetical prote	
7	191	20.5	255	2	E84899	hypothetical prote	
8	182	19.5	271	2	T13013	hypothetical prote	
9	163	17.5	275	2	T05595	hypothetical prote	
10	147	15.8	393	2	S67763	probable membrane	
11	144.5	15.5	242	2	B85016	hypothetical prote	
12	131	14.1	183	2	A84527	hypothetical prote	
13	127.5	13.7	295	2	S59439	probable membrane	

14	124	13.3	206	2	T01153	probable seed matu
15	109.5	11.8	264	2	T47948	hypothetical prote
16	104.5	11.2	203	2	T47571	hypothetical prote
17	95	10.2	288	2	B90043	conserved hypothet
18	94.5	10.2	458	2	A72258	hypothetical prote
19	93	10.0	160	2	C84422	hypothetical prote
20	92.5	9.9	527	2	A84645	probable cytochrom
21	88.5	9.5	405	2	H71692	hypothetical prote
22	88	9.5	224	2	D71915	hydrogenase, cytoc
23	87.5	9.4	296	2	S46018	probable membrane
24	85.5	9.2	442	2	C75057	hypothetical prote
25	85.5	9.2	823	2	H83724	hypothetical prote
26	85.5	9.2	1065	2	E69795	acriflavin resista
27	85	9.1	224	1	A64599	hydrogenase (EC 1.
28	85	9.1	459	2	G86264	F3F19 hypothetical
29	85	9.1	468	2	A38223	nicotinic acetylch
30	85	9.1	1055	2	H90023	hypothetical prote
31	84.5	9.1	151	2	G96705	unknown protein, 7
32	84.5	9.1	457	2	H85095	hypothetical prote
33	84.5	9.1	464	2	C70414	NADH2 dehydrogenas
34	84.5	9.1	677	2	F95232	immunity protein,
35	84.5	9.1	680	2	H98096	conserved hypothet
36	84	9.0	299	2	B69155	hypothetical prote
37	82.5	8.9	570	2	S52765	secD protein - Str
38	82.5	8.9	955	2	T33040	hypothetical prote
39	82	8.8	589	2	F64201	transport ATP-bind
40	81.5	8.8	324	2	AE1700	phospho-N-acetylm
41	81.5	8.8	369	2	H90587	hypothetical prote
42	81.5	8.8	598	2	T14886	leukotoxin express
43	81.5	8.8	822	2	T41622	probable ABC trans
44	81.5	8.8	937	2	T41400	probable peroxisom
45	81	8.7	537	2	G82873	conserved hypothet

ALIGNMENTS

RESULT 1

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: I60904

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865.

A;Map position: 14q21-14q22

Query Match 73.3%; Score 682; DB 2; Length 208;
Best Local Similarity 68.4%; Pred. No. 3.3e-54;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

```
Qy      3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSVTAYIALALLSVTISFRIYKGVIAIQ 62
          :|||||||:|:|:|: | | | | | :| | | | | :| | | | | :|:|:|
Db      22 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQ 81

Qy      63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLM 122
          |:|||||:|||| |: |:|:| :|:|:| :| |:||||| | | | | | | | | |
Db      82 KTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLM 141

Qy     123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
          |: | | | | | | | | | | :|:|:|:|:|:|:|:| :| | | | | | | | | :|:| | | |
Db     142 WLLTYVGALFNGLTLLLMAVVSMTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 201

Qy     183 GLKRKAE 189
          | | | |
Db     202 GAKRHAE 208
```

RESULT 2

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 421-776 <ROE2>

A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 73.3%; Score 682; DB 2; Length 776;
Best Local Similarity 68.4%; Pred. No. 1.5e-53;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

Qy		3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIIQ	62
		: : : : : : :	
Db		590 IDLLYWDRDIQTGIVEGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ	649
Qy		63 KSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRRLFVDLDLSLKFAVLM	122
		: : : : : :	
Db		650 KTDEGHPPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQLDVSLSKFVLM	709
Qy		123 WVFTYVGALFNGLTLILLALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKI QAKIP	182
		: : : : : : : : : :	
Db		710 WLLTYVGALFNGLTLMLMAVSMFTLPVVVVKHQAQIDQYLGLVRTHINAVVAKI QAKIP	769
Qy		183 GLKRKA E 189	
Db		770 GAKRHA E 776	

RESULT 3

A60021

tropomyosin-related protein, neuronal - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993 #text change 05-Nov-1999

C;Accession: A60021

R;Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991

A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.

A;Reference number: A60021; MUID:91278684; PMID:1647480

A;Accession: A60021

A;Molecule type: mRNA

A;Residues: 1-267 <WIE>

A;Cross-references: EMBL:X52817; NID:q456549; PIDN:CAA37001.1; PID:q456550

C;Comment: This neuronal-specific mRNA was identified by hybridization to an

alpha-tropomyosin probe but does not show homology in amino acid sequence.

Query Match 71.4%; Score 665; DB 2; Length 267;

Best Local Similarity 67.2%; Pred. No. 1.5e-52;

Matches 123; Conservative 33; Mismatches 27; Indels 0; Gaps 0;

Qy	3	VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ	62
		: : : : : : : :	
Db	13	IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ	72
Qy	63	KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDLDVDSLKFVILM	122
		: : : : : : :: : :	
Db	73	KTDEGHPFKAYLELEITLSQEIQKYTDCLQLYNSTLKELRRLFLVQDLVDLSLKFVILM	132
Qy	123	WVFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKIQAKIP	182
		: : : : : : : : : : :: :	
Db	133	WLLTYVGALFNGLTLLLMAVVSMTLPVVVVKHQAVDQYLGLVRTHINTVVAKIQAQIP	192
Qy	183	GLK	185
		:	
Db	193	GAR	195

RESULT 4

T26216

hypothetical protein W06A7.3c - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T26216
 R;Ainscough, R.
 submitted to the EMBL Data Library, August 1996
 A;Reference number: Z20173
 A;Accession: T26216
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2484 <WIL>
 A;Cross-references: EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c
 A;Experimental source: clone W06A7
 C;Genetics:
 A;Gene: CESP:W06A7.3c
 A;Map position: 5
 A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 36.0%; Score 335; DB 2; Length 2484;
 Best Local Similarity 33.7%; Pred. No. 1.1e-21;
 Matches 62; Conservative 46; Mismatches 76; Indels 0; Gaps 0;

```

Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
      |:|::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2289 VLDVIYWRDAKSAIVLSLALLVLFVLAKYPLLTVVVTYSLLLALGAAAGFRVFKKVEAQI 2348

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2349 KKTDSHPFSEILAQDLTLPQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFGVLV 2408

Qy      122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
      :| | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      2409 LWSLTYIASWFSGFTLAILGLLVFSPKVPKYESNQEAIDPHLATISGHLKNVQNIIDEKL 2468

Qy      182 PGLK 185
      | | :
Db      2469 PFLR 2472

```

RESULT 5

T26215

hypothetical protein W06A7.3a - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T26215
 R;Ainscough, R.
 submitted to the EMBL Data Library, August 1996
 A;Reference number: Z20173
 A;Accession: T26215
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2607 <WIL>
 A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a
 A;Experimental source: clone W06A7
 C;Genetics:
 A;Gene: CESP:W06A7.3a
 A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;
2586/2

Query Match 36.0%; Score 335; DB 2; Length 2607;
Best Local Similarity 33.7%; Pred. No. 1.2e-21;
Matches 62; Conservative 46; Mismatches 76; Indels 0; Gaps 0;

```
Qy      2 VDDLlyWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
      |:|::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2412 VLDVIYWRDAKSAIVLSLALLVLFVLAKYPLLTVVITYSLLLALGAAAGFRVFKKVEAQI 2471

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAVL 121
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2472 KKTDEHPFSEILAQDLTLPQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFLV 2531

Qy      122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
      :| | | : | : | | | | | | | | | | | | | | | | | | | | | |
Db      2532 LWSLTYIASWFSGFTLAILGLLVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKL 2591

Qy      182 PGLK 185
      | | :
Db      2592 PFLR 2595
```

RESULT 6

T26213

hypothetical protein W06A7.3b - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26213

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26213

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-222 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3b

A;Map position: 5

A;Introns: 27/1; 77/2; 201/2

Query Match 35.9%; Score 334; DB 2; Length 222;
Best Local Similarity 33.2%; Pred. No. 8.6e-23;
Matches 61; Conservative 47; Mismatches 76; Indels 0; Gaps 0;

```
Qy      2 VDDLlyWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
      :|:|::| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      27 ILDVIYWRDAKSAIVLSLALLVLFVLAKYPLLTVVITYSLLLALGAAAGFRVFKKVEAQI 86

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAVL 121
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      87 KKTDEHPFSEILAQDLTLPQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFLV 146

Qy      122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
```

```

      :| ||: : |:| || || |: :||| :|| :| || :| : :|: | |:
Db      147 LWSLTYYIASWFSGFTLAILGLLGVFSPKVVYESNQEAIDPHLATISGHLKNVQNIIDEKL 206

Qy      182 PGLK 185
      | |:
Db      207 PFLR 210

```

RESULT 7

E84899

hypothetical protein At2g46170 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: E84899

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84899

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-255 <STO>

A;Cross-references: GB:AE002093; NID:g3702332; PIDN:AAC62889.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g46170

A;Map position: 2

```

Query Match          20.5%; Score 191; DB 2; Length 255;
Best Local Similarity 27.9%; Pred. No. 8e-10;
Matches 55; Conservative 40; Mismatches 78; Indels 24; Gaps 6;

```

```

Qy      4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 61
      |: ||| |:| | | :||| | | : :|: :|:| | :| :|
Db      70 DVFLWRDKKLSGAVLGVATAIWVLFELVEYHLLSLLCHISILALG---GLFLWSNAHTLI 126

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
      |: | | | | | | | | | | | | | | | | | | | |
Db      127 NKTSPQIP-----EIHVP EEAF LVVASSLRNELNQAFVILRSIALGRDLKKFLMVVVG 179

Qy      122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAM----- 174
      |: : || || ||| : : | :||:| |:| :| | | |:|
Db      180 LWIISVVGWNWFNFTLVYICFVILHTVPMLYEKHEDKVD---PLAEKAMKELQKQYVVFD 236

Qy      175 AKIQAKIP--GLKRKAE 189
      |: :||| || ||:
Db      237 EKVLSKIPIASLKAKAK 253

```

RESULT 8

T13013

hypothetical protein F8L21.10 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-Oct-1999
 C;Accession: T13013
 R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.
 submitted to the Protein Sequence Database, July 1999
 A;Reference number: Z17587
 A;Accession: T13013
 A;Molecule type: DNA
 A;Residues: 1-271 <BEV>
 A;Cross-references: EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.10
 A;Experimental source: cultivar Columbia; BAC clone F8L21
 C;Genetics:
 A;Gene: ATSP:F8L21.10
 A;Map position: 4
 A;Introns: 85/1; 145/2; 192/3; 216/1

Query Match 19.5%; Score 182; DB 2; Length 271;
 Best Local Similarity 26.1%; Pred. No. 5.6e-09;
 Matches 47; Conservative 42; Mismatches 79; Indels 12; Gaps 3;

```

Qy      4 DLLYWRDIKKTGVVFGAS--LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
      | : | | : | || | : : | | : : : : : | : | : : |
Db      87 DIFMWKDKKMSGGVFGGATVAWVLFELMEYHLLTLLCHVMIVALAVLF---LWSNATMFI 143

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
      || | | | | | | | : : : : : | | | | : | : |
Db      144 HKSPPKIP-----EVHIPEEPLLQLASGLRIEINRGISLREIASGRDIKKFLSAIAG 196

Qy      122 MWVFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
      : || : : | : : || | : || : || : || : || : : | | : | | : || :
Db      197 LWVLSILGGCYSFLTLYIALVLLFTVPLFYDKYEDKVDSYGEKAMAEKKQYAVLDAKV 256

```

RESULT 9

T05595

hypothetical protein F9D16.100 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
 C;Accession: T05595
 R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller, C.
 submitted to the Protein Sequence Database, February 1999
 A;Reference number: Z15419
 A;Accession: T05595
 A;Molecule type: DNA
 A;Residues: 1-275 <BEV>
 A;Cross-references: EMBL:AL035394
 A;Experimental source: cultivar Columbia; BAC clone F9D16
 C;Genetics:
 A;Map position: 4
 A;Introns: 89/1; 149/2; 196/3; 220/1
 A;Note: F9D16.100

Query Match 17.5%; Score 163; DB 2; Length 275;
 Best Local Similarity 26.0%; Pred. No. 2.9e-07;

Matches 50; Conservative 42; Mismatches 82; Indels 18; Gaps 5;

```
Qy      4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
      |: |:: | :| | | : :: | : :::: : : : :|:| : : |
Db      91 DIFMWKNKKMSGGVLGGATAAWVVFELMEYHLLTLLCHVMIVVLAVLF---LWSNATMFI 147

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
      || | | | | | : : : : : | | : | | |
Db      148 NKSPPKIP-----EVHIPEEPILQLASGLRIEINRGFSSLREIASGRDLKKFLIAIAG 200

Qy      122 MWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMA----KI 177
      :|| : :| || || :||: ||:| :|::: :| | :| | | :
Db      201 LWVLSILGGCFNFLTLAYIALVLLFTVPLAYDKYEDKVDPLGEKAMIELKKQYAVLDEKV 260

Qy      178 QAKIP--GLKRK 187
      :||| || |
Db      261 LSKIPLGPLKNK 272
```

RESULT 10

S67763

probable membrane protein YDL204w - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein D1062

C;Species: *Saccharomyces cerevisiae*

C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002

C;Accession: S67763

R;Schmidt, E.R.; Bahr, A.; Kraemer, C.; Hankeln, T.; Moeller-Rieker, S.
submitted to the Protein Sequence Database, July 1996

A;Reference number: S67756

A;Accession: S67763

A;Molecule type: DNA

A;Residues: 1-393 <SCH>

A;Cross-references: EMBL:Z74252; NID:g1431337; PID:e253109; PID:g1431338;

GSPDB:GN00004; MIPS:YDL204w

A;Experimental source: strain S288C

C;Genetics:

A;Gene: MIPS:YDL204w

A;Cross-references: SGD:S0002363

A;Map position: 4L

C;Keywords: transmembrane protein

F;50-66/Domain: transmembrane #status predicted <TM1>

F;150-166/Domain: transmembrane #status predicted <TM2>

Query Match 15.8%; Score 147; DB 2; Length 393;

Best Local Similarity 27.0%; Pred. No. 1.2e-05;

Matches 47; Conservative 34; Mismatches 51; Indels 42; Gaps 5;

```
Qy      5 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKS 64
      |:|| : |:| | |:| || | :::|| | :| :
Db      33 LIYWTNPSKSGASFAATLVSLILRNVNVISVLLKIGYMLFVS----- 76

Qy      65 DEGHPFRAYLESEVAISEELVQKY----SNSALG----HVNCTIKELRRLFLVDDLVDLSL 116
      | | :| : :| : : | :| | :| || :| : |
Db      77 -----FAVELSTKVLFDKGVVSRFGMQESPDLVGVLKPHID---RELDRLPALEDRIKRL 128

Qy      117 KFA-----VLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQID 160
      || | : : |:| : |:| : | |:| :| :| :| :|
```

Db 129 VFAHRTRNNFTIGVSLYFLHGLFAIFSMNTVLMITTIFLYTVPLIYDRKQARID 182

RESULT 11

B85016

hypothetical protein AT4g01230 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C;Accession: B85016

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor, Washington University in St Louis and PE Biosystems Arabidopsis Sequencing Consortium.

Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: B85016

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-242 <STO>

A;Cross-references: GB:NC_001268; NID:g7267620; PIDN:CAB80932.1; GSPDB:GN00140

C;Genetics:

A;Gene: AT4g01230

A;Map position: 4

Query Match 15.5%; Score 144.5; DB 2; Length 242;
Best Local Similarity 24.7%; Pred. No. 1.2e-05;
Matches 47; Conservative 47; Mismatches 67; Indels 29; Gaps 6;

Qy 4 DLLYWRDIKKTGVVFGASLFLLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKG 56

Db 70 DVLLWRDKKVT-----LGLLSAVTVIWLFLFGFGRRLLTSLCRGSILFLLLSF-LWS- 120

Qy 57 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSL 116

Db 121 --NALNKSPEN-----MMDIYIPEKPLLQAASAMTFELNCAFATLRSIALERDIKNFV 171

Qy 117 KFAVLMWVFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLA----NKNVKD 172

Db 172 MAVIGLWLVSIGNWFSFLSLLYICFVLIHTVPMLEYEYEDIDPIAEKAVIEMKKHYQV 231

Qy 173 AMAKIQAKIP 182

Db 232 FEAFLSKIP 241

RESULT 12

A84527

hypothetical protein At2g15280 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84527

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver,

G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: A84527
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-183 <STO>
 A;Cross-references: GB:AE002093; NID:g4662633; PIDN:AAD26905.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g15280
 A;Map position: 2

Query Match 14.1%; Score 131; DB 2; Length 183;
 Best Local Similarity 24.0%; Pred. No. 0.00014;
 Matches 43; Conservative 38; Mismatches 80; Indels 18; Gaps 4;

```

Qy      8 WRDIKKTGVVFGAS-----LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 62
      |:: :  :: |::  ||      : | |      :  ||| | |  | |
Db      2 WKNRRGGFLLLGSTLLWFLFEKCGYSFFPFV-----VNTQLLSVVILFLWAKSAI---- 52

Qy     63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
      :  |  ||  |::| |  :::  : |  :  |:: :  : :|::
Db     53 LFNRPMPQLPNLE----ITEEFVFMVADAIRVWINTVLAVAREIYVGRNAKQLFRVSVVL 108

Qy    123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
      |  ::||  | ||:| | ::  : | :|||:|  ||  | | :: :  ||  ::
Db    109 WTVSFVGNFLNFLTILYLGVVLSLLIPFLYERYQDLIDEKLSLTHRVIQTQYRKIDERL 167
  
```

RESULT 13

S59439

probable membrane protein YDR233c - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein YD9934.17c

C;Species: *Saccharomyces cerevisiae*

C;Date: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 19-Apr-2002

C;Accession: S59439

R;Murphy, L.; Harris, D.

submitted to the EMBL Data Library, March 1995

A;Reference number: S59423

A;Accession: S59439

A;Molecule type: DNA

A;Residues: 1-295 <MUR>

A;Cross-references: EMBL:Z48612; NID:g728671; PID:g728688; GSPDB:GN00004;

MIPS:YDR233c

A;Experimental source: strain AB972

C;Genetics:

A;Gene: MIPS:YDR233c

A;Cross-references: SGD:S0002641

A;Map position: 4R

C;Keywords: transmembrane protein

F;40-56/Domain: transmembrane #status predicted <TM1>

F;146-162/Domain: transmembrane #status predicted <TM2>

Query Match 13.7%; Score 127.5; DB 2; Length 295;

Best Local Similarity 21.6%; Pred. No. 0.0005;
Matches 45; Conservative 43; Mismatches 69; Indels 51; Gaps 5;

```

Qy      4 DLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQK 63
      ||| ||: :|| || || || | ::: :| :| | | : :
Db      22 DLLLWRNPVQTGKYFGGSLALLLILKKVNLITFFLKVAYTILETT-----GSIEFV-- 72

Qy      64 SDEGHPFRAYLESEVAISEELVQKY-----SNSALGHVNCTIKEL-----RRLFL 108
      |:: : : |: || : |:: :|:| | :
Db      73 -----SKLFLGQGLITKYGPKECPNIAGFIKPHIDEALKQLPVFQAHIRKTVF 120

Qy      109 VDDLVDLSLKFAVLMWVFTYVGALENGLTLLILALISLFSVPVIYERHQAQID----- 160
      : | || :: : | : |:: :| | |::||| : :||
Db      121 AQVPKHTEKTAVALFLLHKFFSWFSIWTFIVFVADIFTFTLPVIYHSYKHEIDATVAQGVE 180

Qy      161 -----HYLGLANKNVKDAMAKIQAKI 181
      : :| : | : |::|:
Db      181 ISKQKTQEF SQMACEKTKPYLDKVESKL 208

```

RESULT 14

T01153

probable seed maturation protein [imported] - Arabidopsis thaliana

N;Alternate names: hypothetical protein F27L4.17

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001

C;Accession: T01153; T02426; C84627

R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.

submitted to the EMBL Data Library, June 1998

A;Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.

A;Reference number: Z14198

A;Accession: T01153

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-206 <ROU>

A;Cross-references: EMBL:AC003040; NID:g3242700; PID:g3242725

A;Experimental source: cultivar Columbia

R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.

submitted to the EMBL Data Library, May 1998

A;Description: Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence.

A;Reference number: Z14658

A;Accession: T02426

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-206 <RO2>

A;Cross-references: EMBL:AC004482; NID:g3152602; PIDN:AAC17096.1; PID:g3152617

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: C84627

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-206 <STO>

A;Cross-references: GB:AE002093; NID:g3152617; PIDN:AAC17096.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g23640; F26B6.29; F27L4.17

A;Map position: 2

A;Introns: 14/1; 76/2; 147/1

C;Superfamily: *Arabidopsis thaliana* hypothetical protein F27L4.17

Query Match 13.3%; Score 124; DB 2; Length 206;
Best Local Similarity 24.4%; Pred. No. 0.00069;
Matches 48; Conservative 44; Mismatches 75; Indels 30; Gaps 8;

```
QY      2 VVDLLYWRDIKK--TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQ 59
      | | : | | | : : : | : | | | | : : : : | : | : | : : : :
Db      16 VEDIYLWRRKKLAFSTLLVSTSTWILLSFYGFTTITIVSWIGIAVVS MIF---LWGSLLR 72

QY      60 AIQKSDEGHPFRAYLESEVA---ISEELVQKYSNSALGHVNCTI---KELRRLFLVDDLV 113
      : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      73 LLSK-----VEPELSGLEVSEEFVTVRS-----CRMLMEEMVRWMFRVGAES 116

QY      114 DSLKFA--VL-MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNV 170
      : | | | | | : : : | | : | | : | : | : | : | : | : |
Db      117 EWFVFARTVLGFWILSRIGNLLDFHTCLFIGLVMGLTVPKLWEEYGDQIQKHLGSLKDKS 176

QY      171 KDAMAKIQAKIPGLKRK 187
      | | | | : | |
Db      177 KGAYNTTHEKILEMKNK 193
```

RESULT 15

T47948

hypothetical protein F2A19.160 - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C;Accession: T47948

R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.

submitted to the Protein Sequence Database, January 2000

A;Reference number: Z24480

A;Accession: T47948

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-264 <DEH>

A;Cross-references: EMBL:AL132962

A;Experimental source: cultivar Columbia; BAC clone F2A19

C;Genetics:

A;Map position: 3

A;Introns: 68/1; 128/2; 164/1; 210/1

A;Note: F2A19.160

Query Match 11.8%; Score 109.5; DB 2; Length 264;
 Best Local Similarity 25.2%; Pred. No. 0.019;
 Matches 55; Conservative 37; Mismatches 69; Indels 57; Gaps 14;

```

Qy      4 DILYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYI-----ALALLSVTISFRIYK 55
      |: ||| |: | | ::::| | : :|: :| || ||| :| : |
Db      70 DVFLWRDKKLSASVLGVATAIWVLFELVEYHFLSLVCHILIFALAAFLLSNAHAF-MNK 128

Qy      56 GVIQ-----AIQKSDEG-----HPFRAYLESEVAISEELVQK-YSN-SALGHVNCTIKE 102
      |          ::::| | | || || ||:| | | :| | |
Db      129 GTFPYDCFCTEKRAEPGLCYFKEHCLRKGLLE---ISHELIQSTYETFSIMGFVTRT--- 182

Qy      103 LRRFLVDDLVDLSLKFAVL--MWVFTYVGALFNG--LTLLILALISLFSVPVIYERHQAQ 158
      |: : | :| | : || : | :||::||: :
Db      183 -----SIYIGISGGFWAVDNLGC---GKLVQLLDSCFVVLHTVPMLEYEKHEDK 227

Qy      159 IDHYLGLANKNVKDAM-----AKIQAKIPGLKRKAE 189
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Db      228 VD---PVAEKTILKELKKHYMVFDEKVL SKLPVASLKAK 262

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Search completed: September 29, 2004, 18:16:05
 Job time : 6.62587 secs

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:16:15 ; Search time 20.2878 Seconds
(without alignments)
2997.869 Million cell updates/sec

Title: US-09-830-972-29_COPY_990_1178
Perfect score: 931
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	931	100.0	1192	9	US-09-789-386-2	Sequence 2, Appli
2	931	100.0	1192	9	US-09-758-140-6	Sequence 6, Appli
3	931	100.0	1192	9	US-09-893-348-23	Sequence 23, Appl
4	931	100.0	1192	9	US-09-972-599A-6	Sequence 6, Appli
5	931	100.0	1192	12	US-10-267-502-429	Sequence 429, App
6	931	100.0	1192	14	US-10-060-036-71	Sequence 71, Appl
7	931	100.0	1192	16	US-10-327-213-9	Sequence 9, Appli
8	931	100.0	1192	16	US-10-466-258-9	Sequence 9, Appli
9	927	99.6	199	9	US-09-893-348-25	Sequence 25, Appl
10	927	99.6	199	12	US-10-660-946-1	Sequence 1, Appli
11	927	99.6	373	9	US-09-789-386-6	Sequence 6, Appli
12	927	99.6	373	9	US-09-765-205-6	Sequence 6, Appli
13	927	99.6	373	9	US-09-893-348-24	Sequence 24, Appl
14	927	99.6	373	12	US-10-408-967-8	Sequence 8, Appli
15	927	99.6	373	14	US-10-060-036-72	Sequence 72, Appl
16	927	99.6	373	16	US-10-466-258-4	Sequence 4, Appli
17	924	99.2	1192	12	US-10-408-967-7	Sequence 7, Appli
18	920	98.8	199	12	US-10-408-967-9	Sequence 9, Appli
19	918	98.6	199	12	US-09-978-360A-467	Sequence 467, App
20	908	97.5	1163	9	US-09-893-348-18	Sequence 18, Appl
21	905	97.2	379	14	US-10-205-194-164	Sequence 164, App
22	904.5	97.2	1163	12	US-10-267-502-431	Sequence 431, App
23	904	97.1	199	9	US-09-893-348-21	Sequence 21, Appl
24	904	97.1	360	9	US-09-893-348-20	Sequence 20, Appl
25	886	95.2	199	16	US-10-466-258-11	Sequence 11, Appl
26	682	73.3	208	12	US-10-660-946-7	Sequence 7, Appli
27	682	73.3	356	12	US-10-660-946-6	Sequence 6, Appli
28	682	73.3	776	12	US-10-660-946-5	Sequence 5, Appli
29	682	73.3	776	12	US-10-267-502-430	Sequence 430, App
30	681	73.1	777	14	US-10-205-219-93	Sequence 93, Appl
31	681	73.1	780	12	US-10-267-502-432	Sequence 432, App
32	665	71.4	267	12	US-10-660-946-8	Sequence 8, Appli
33	665	71.4	267	14	US-10-205-194-127	Sequence 127, App
34	624.5	67.1	236	9	US-09-729-674-20	Sequence 20, Appl
35	624.5	67.1	236	9	US-09-765-205-26	Sequence 26, Appl
36	624.5	67.1	236	12	US-10-408-967-2	Sequence 2, Appli
37	624.5	67.1	266	12	US-10-276-774-2330	Sequence 2330, Ap
38	624.5	67.1	269	14	US-10-106-698-6222	Sequence 6222, Ap
39	619.5	66.5	593	15	US-10-108-260A-2892	Sequence 2892, Ap
40	541.5	58.2	168	10	US-09-809-391-563	Sequence 563, App
41	541.5	58.2	168	10	US-09-882-171-563	Sequence 563, App
42	541.5	58.2	168	12	US-10-164-861-563	Sequence 563, App
43	520	55.9	222	12	US-10-267-502-428	Sequence 428, App
44	512	55.0	241	12	US-10-660-946-3	Sequence 3, Appli
45	508.5	54.6	234	12	US-10-424-599-200840	Sequence 200840,

ALIGNMENTS

RESULT 1

US-09-789-386-2

; Sequence 2, Application US/09789386

; Patent No. US20020010324A1

; GENERAL INFORMATION:

; APPLICANT: MICHALOVICH, DAVID

; APPLICANT: PRINJHA, RABINDER KUMAR
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP-30165-C1
 ; CURRENT APPLICATION NUMBER: US/09/789,386
 ; CURRENT FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: U.K. 9916898.1
 ; PRIOR FILING DATE: 1999-07-19
 ; PRIOR APPLICATION NUMBER: U.K. 9816024.5
 ; PRIOR FILING DATE: 1998-07-22
 ; PRIOR APPLICATION NUMBER: US 09/359,208
 ; PRIOR FILING DATE: 1999-07-22
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 1192
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-789-386-2

Query Match 100.0%; Score 931; DB 9; Length 1192;
 Best Local Similarity 100.0%; Pred. No. 1.6e-86;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60
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 Db 1004 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1063
 Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
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 Db 1064 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123
 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
 |||
 Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183
 Qy 181 IPGLKRKAE 189
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 Db 1184 IPGLKRKAE 1192

RESULT 2

US-09-758-140-6

; Sequence 6, Application US/09758140

; Patent No. US20020012965A1

; GENERAL INFORMATION:

; APPLICANT: Strittmatter, Stephen M.

; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth

; FILE REFERENCE: 44574-5073-US

; CURRENT APPLICATION NUMBER: US/09/758,140

; CURRENT FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: US 60/175,707

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: US 60/207,366

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 60/236,378

; PRIOR FILING DATE: 2000-09-29

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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-140-6
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Qy	61	IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAV	120
Db	1064	IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAV	1123
Qy	121	LMWVFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK	180
Db	1124	LMWVFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK	1183
Qy	181	IPGLKRKAE	189
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; ORGANISM: Homo sapiens
US-09-893-348-23

Query Match 100.0%; Score 931; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLVDLKFV 1123

Qy      121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
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Qy      181 IPGLKRKAE 189
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Db      1184 IPGLKRKAE 1192
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RESULT 4

US-09-972-599A-6

; Sequence 6, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

Query Match 100.0%; Score 931; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      181 IPGLKRKAE 189
Db      1184 IPGLKRKAE 1192

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RESULT 5

US-10-267-502-429

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; Sequence 429, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502.
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-429

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Query Match      100.0%; Score 931; DB 12; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123
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Db      1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183
Qy      181 IPGLKRKAE 189
Db      1184 IPGLKRKAE 1192

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RESULT 6

; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-213-9

Query Match 100.0%; Score 931; DB 16; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1063

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLQKFAV 120
|
Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLQKFAV 1123

Qy 121 LMWVFYTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
|
Db 1124 LMWVFYTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy 181 IPGLKRKAE 189
|
Db 1184 IPGLKRKAE 1192

RESULT 8

US-10-466-258-9
; Sequence 9, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-258-9

Query Match 100.0%; Score 931; DB 16; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60
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Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1063

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLQKFAV 120
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Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123

Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
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Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy 181 IPGLKRKAE 189
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Db 1184 IPGLKRKAE 1192

RESULT 9

US-09-893-348-25
 ; Sequence 25, Application US/09893348
 ; Patent No. US20020072493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal
 ; APPLICANT: COHEN, Irun R.
 ; APPLICANT: BESERMAN, Pierre
 ; APPLICANT: MOSONEGO, Alon
 ; APPLICANT: MOALEM, Gila
 ; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
 THEIR USES
 ; FILE REFERENCE: EIS-SCHWARTZ=2A
 ; CURRENT APPLICATION NUMBER: US/09/893,348
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US 09/314,161
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: US 09/218,277
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: PCT/US98/14715
 ; PRIOR FILING DATE: 1998-07-21
 ; PRIOR APPLICATION NUMBER: IL 124500
 ; PRIOR FILING DATE: 1998-05-19
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 25
 ; LENGTH: 199
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-893-348-25

Query Match 99.6%; Score 927; DB 9; Length 199;
 Best Local Similarity 100.0%; Pred. No. 3.8e-87;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 71

Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
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Db 72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 131

Qy 122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
 |||

Db 132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy 182 PGLKRKAE 189
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Db 192 PGLKRKAE 199

RESULT 10

US-10-660-946-1

; Sequence 1, Application US/10660946
; Publication No. US20040063131A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Au-Young, Janice
; Goli, Surya K.
; Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/660,946
; FILING DATE: 12-Sep-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/228,213A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/700,607
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-660-946-1

Query Match 99.6%; Score 927; DB 12; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.8e-87;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 71

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 131

Qy     122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy     182 PGLKRKAE 189
          |||||||
Db     192 PGLKRKAE 199
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RESULT 11

US-09-789-386-6
; Sequence 6, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6

Query Match 99.6%; Score 927; DB 9; Length 373;
Best Local Similarity 100.0%; Pred. No. 8.8e-87;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 245

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 305
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Qy 122 MWVFTYVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
 |||
 Db 306 MWVFTYVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 365
 Qy 182 PGLKRKAE 189
 |||
 Db 366 PGLKRKAE 373

RESULT 12

US-09-765-205-6
 ; Sequence 6, Application US/09765205
 ; Patent No. US20020034800A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Li
 ; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
 ; FILE REFERENCE: 1458.004/200130.449
 ; CURRENT APPLICATION NUMBER: US/09/765,205
 ; CURRENT FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US/09/212,440
 ; PRIOR FILING DATE: 1998-12-16
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 373
 ; TYPE: PRT
 ; ORGANISM: human
 US-09-765-205-6

Query Match 99.6%; Score 927; DB 9; Length 373;
 Best Local Similarity 100.0%; Pred. No. 8.8e-87;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 61
 |||
 Db 186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 245
 Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
 |||
 Db 246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 305
 Qy 122 MWVFTYVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
 |||
 Db 306 MWVFTYVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 365
 Qy 182 PGLKRKAE 189
 |||
 Db 366 PGLKRKAE 373

RESULT 13

US-09-893-348-24
 ; Sequence 24, Application US/09893348
 ; Patent No. US20020072493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal

```

; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-24

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Query Match          99.6%; Score 927; DB 9; Length 373;
Best Local Similarity 100.0%; Pred. No. 8.8e-87;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 245

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 305

Qy      122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      306 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 365

Qy      182 PGLKRKAE 189
        ||||||||
Db      366 PGLKRKAE 373

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```

RESULT 14
US-10-408-967-8
; Sequence 8, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Yan, Riqiang
; APPLICANT: Lu, Yifeng
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
; FILE REFERENCE: 00925
; CURRENT APPLICATION NUMBER: US/10/408,967

```

; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-967-8

Query Match 99.6%; Score 927; DB 12; Length 373;
Best Local Similarity 100.0%; Pred. No. 8.8e-87;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 245

Qy     62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 305

Qy    122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 365

Qy    182 PGLKRKAE 189
        |||||||
Db    366 PGLKRKAE 373
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RESULT 15

US-10-060-036-72

; Sequence 72, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-72

Query Match 99.6%; Score 927; DB 14; Length 373;
Best Local Similarity 100.0%; Pred. No. 8.8e-87;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
 |||
 Db 186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 245
 Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLVLKFAVL 121
 |||
 Db 246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLVLKFAVL 305
 Qy 122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
 |||
 Db 306 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 365
 Qy 182 PGLKRKAE 189
 |||
 Db 366 PGLKRKAE 373

Search completed: September 29, 2004, 18:48:19
 Job time : 21.2878 secs

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:06:43 ; Search time 14.8689 Seconds
(without alignments)
4010.587 Million cell updates/sec

Title: US-09-830-972-29_COPY_990_1178
Perfect score: 931
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

1	931	100.0	986	4	Q8IUA4	Q8iua4 homo sapien
2	928	99.7	392	4	Q96B16	Q96b16 homo sapien
3	915	98.3	578	11	Q80W95	Q80w95 mus musculu
4	915	98.3	639	11	Q8K290	Q8k290 mus musculu
5	915	98.3	1046	11	Q8BGK7	Q8bgk7 mus musculu
6	915	98.3	1162	11	Q8BGM9	Q8bgm9 mus musculu
7	912	98.0	375	11	Q8BHF5	Q8bhf5 mus musculu
8	911	97.9	356	11	Q8BH78	Q8bh78 mus musculu
9	904.5	97.2	1163	11	Q8K3G8	Q8k3g8 mus musculu
10	901	96.8	184	6	Q7YRW9	Q7yrw9 bos taurus
11	900.5	96.7	357	11	Q8K3G7	Q8k3g7 mus musculu
12	882	94.7	199	13	Q7T224	Q7t224 gallus gall
13	867	93.1	179	6	Q9GM33	Q9gm33 macaca fasc
14	750	80.6	214	13	Q7T222	Q7t222 carassius a
15	682	73.3	199	4	Q9BQ59	Q9bq59 homo sapien
16	681	73.1	780	11	Q8K4S4	Q8k4s4 mus musculu
17	681	73.1	780	11	Q8K0T0	Q8k0t0 mus musculu
18	672	72.2	760	13	Q90638	Q90638 gallus gall
19	668	71.8	208	13	Q90637	Q90637 gallus gall
20	665	71.4	267	11	Q63765	Q63765 rattus sp.
21	623.5	67.0	236	11	Q8VBU0	Q8vbu0 rattus norv
22	623.5	67.0	237	11	Q8C6D5	Q8c6d5 mus musculu
23	622.5	66.9	643	11	Q8CCU2	Q8ccu2 mus musculu
24	583	62.6	221	13	Q7ZUD6	Q7zud6 brachydanio
25	521	56.0	224	5	Q9VMW1	Q9vmw1 drosophila
26	520	55.9	222	5	Q9VMW4	Q9vmw4 drosophila
27	520	55.9	234	5	Q9VMW3	Q9vmw3 drosophila
28	520	55.9	595	5	Q9VMV9	Q9vmv9 drosophila
29	518	55.6	202	5	Q9VMW2	Q9vmw2 drosophila
30	343	36.8	107	13	Q7T223	Q7t223 carassius a
31	335	36.0	2484	5	Q9U347	Q9u347 caenorhabdi
32	335	36.0	2607	5	Q23187	Q23187 caenorhabdi
33	334	35.9	222	5	Q23188	Q23188 caenorhabdi
34	199.5	21.4	154	5	Q9VIB7	Q9vib7 drosophila
35	199.5	21.4	158	5	Q24199	Q24199 drosophila
36	191	20.5	255	10	O82352	O82352 arabidopsis
37	187	20.1	255	10	Q9SH59	Q9sh59 arabidopsis
38	182	19.5	271	10	Q9SUT9	Q9sut9 arabidopsis
39	165.5	17.8	197	5	Q9NJS2	Q9njs2 leishmania
40	164	17.6	257	10	Q9FFS0	Q9ffs0 arabidopsis
41	163	17.5	275	10	Q9SUR3	Q9sur3 arabidopsis
42	159	17.1	200	10	Q9LT71	Q9lt71 arabidopsis
43	158	17.0	279	10	Q9AWY7	Q9awy7 oryza sativ
44	157	16.9	200	10	Q8LAT8	Q8lat8 arabidopsis
45	154.5	16.6	192	10	Q7XR59	Q7xr59 oryza sativ

ALIGNMENTS

RESULT 1

Q8IUA4

ID Q8IUA4 PRELIMINARY; PRT; 986 AA.
AC Q8IUA4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE RNT4 (RTN4).
 GN RTN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22376540; PubMed=12488097;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL J. Mol. Biol. 325:299-323(2003).
 DR EMBL; AY102285; AAM64244.1; -.
 DR EMBL; AY123245; AAM64249.1; -.
 DR EMBL; AY123246; AAM64250.1; -.
 DR EMBL; AY123247; AAM64251.1; -.
 DR EMBL; AY123248; AAM64252.1; -.
 DR EMBL; AY123249; AAM64253.1; -.
 DR EMBL; AY123250; AAM64254.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

Query Match 100.0%; Score 931; DB 4; Length 986;
 Best Local Similarity 100.0%; Pred. No. 2.7e-75;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60
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 Db 798 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 857

 Qy 61 IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAV 120
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 Db 858 IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAV 917

 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
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 Db 918 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 977

Qy 181 IPGLKRKAE 189
|||||
Db 978 IPGLKRKAE 986

RESULT 2

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.
AC Q96B16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (RTN4).
GN RTN4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22376540; PubMed=12488097;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL J. Mol. Biol. 325:299-323(2003).
DR EMBL; BC016165; AAH16165.1; -.
DR EMBL; AY102285; AAM64242.1; -.
DR EMBL; AY102278; AAM64247.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Hypothetical protein.
SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 99.7%; Score 928; DB 4; Length 392;
Best Local Similarity 99.5%; Pred. No. 1.8e-75;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
 :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 204 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 263

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 264 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 323

Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 324 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 383

Qy 181 IPGLKRKAE 189
 |||||||||
 Db 384 IPGLKRKAE 392

RESULT 3
 Q80W95

ID Q80W95 PRELIMINARY; PRT; 578 AA.
 AC Q80W95;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nogo-A (Fragment).
 GN NOGO-A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tozaki H., Hirata T.;
 RT "The partial sequence of mouse nogo-A cDNA clone#4109."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB073672; BAC75974.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 98.3%; Score 915; DB 11; Length 578;
 Best Local Similarity 98.4%; Pred. No. 4.2e-74;
 Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 390 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 449

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 450 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 509

Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180

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          |||
Db      510 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 569
          |||
Qy      181 IPGLKRKAE 189
          |||
Db      570 IPGLKRKAE 578

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RESULT 4

Q8K290

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ID   Q8K290      PRELIMINARY;      PRT;      639 AA.
AC   Q8K290;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032192; AAH32192.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Hypothetical protein.
SQ   SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

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Query Match          98.3%; Score 915; DB 11; Length 639;
Best Local Similarity 98.4%; Pred. No. 4.7e-74;
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
          |||
Db      451 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 510
          |||
Qy      61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
          |||
Db      511 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 570
          |||
Qy      121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
          |||
Db      571 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 630
          |||
Qy      181 IPGLKRKAE 189
          |||
Db      631 IPGLKRKAE 639

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RESULT 5

Q8BGK7

ID Q8BGK7 PRELIMINARY; PRT; 1046 AA.
AC Q8BGK7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RTN4.
GN RTN4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvcJ7;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvcJ7;
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129SvcJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY102280; AAM73502.1; -.
DR EMBL; AY102286; AAM73507.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 98.3%; Score 915; DB 11; Length 1046;
Best Local Similarity 98.4%; Pred. No. 8e-74;
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
|
Db 858 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 917

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
|
Db 918 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 977

Qy 121 LMWVFTYVVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180

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          |||
Db      978 LMWVFTYVGFALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 1037
          |||
Qy      181 IPGLKRKAE 189
          |||
Db      1038 IPGLKRKAE 1046

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RESULT 6

Q8BGM9

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ID   Q8BGM9      PRELIMINARY;      PRT; 1162 AA.
AC   Q8BGM9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102284; AAM73506.1; -.
DR   EMBL; AY102286; AAM73511.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE 1162 AA; 126613 MW; 855697FBEE11781F CRC64;

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Query Match          98.3%; Score 915; DB 11; Length 1162;
Best Local Similarity 98.4%; Pred. No. 9e-74;
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 1033

QY 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1034 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1093

QY 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
 ||||||||||||||||||||||||||||:||||||||||||||||||:|||||||
 Db 1094 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 1153

QY 181 IPGLKRKAE 189
 ||||||||
 Db 1154 IPGLKRKAE 1162

RESULT 7

Q8BHF5

ID Q8BHF5 PRELIMINARY; PRT; 375 AA.
 AC Q8BHF5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RTN4.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvcJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY102282; AAM73504.1; -.
 DR EMBL; AY102286; AAM73509.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match 98.0%; Score 912; DB 11; Length 375;
Best Local Similarity 97.9%; Pred. No. 4.8e-74;
Matches 185; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 60
:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 187 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 246

QY 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAV 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 247 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAV 306

QY 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 307 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 366

QY 181 IPGLKRKAE 189
|||||||||
Db 367 IPGLKRKAE 375

RESULT 8

Q8BH78

ID Q8BH78 PRELIMINARY; PRT; 356 AA.

AC Q8BH78;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., van der Putten H., Schwab M.E.;

RT "Genomic Structure and Functional Characterization of the Promoter

RT Structures of Human and Mouse Nogo/Rtn-4.";

RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., Schwab M.E.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7;

RA Van der Putten H.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.
RC STRAIN=129SvcJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY102281; AAM73503.1; -.
DR EMBL; AY102286; AAM73508.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 97.9%; Score 911; DB 11; Length 356;
Best Local Similarity 98.4%; Pred. No. 5.6e-74;
Matches 185; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VDDLlyWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 61
|||||
Db 169 VDDLlyWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 228
Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
|||||
Db 229 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 288
Qy 122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
|||||:|||||:|||||
Db 289 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKI 348
Qy 182 PGLKRKAE 189
|||||
Db 349 PGLKRKAE 356

RESULT 9

Q8K3G8

ID Q8K3G8 PRELIMINARY; PRT; 1163 AA.
AC Q8K3G8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nogo-A.
GN RTN4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Jin W., Long M., Li R., Ju G.;
RT "Cloning and expression of the mouse Nogo-A protein."
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY114152; AAM77068.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.

DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1163 AA; 126691 MW; 6B5F362799417EA4 CRC64;

Query Match 97.2%; Score 904.5; DB 11; Length 1163;
Best Local Similarity 97.9%; Pred. No. 8e-73;
Matches 186; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIO 59
|||||
Db 974 SVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIO 1033

Qy 60 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFA 119
|||||
Db 1034 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFA 1093

Qy 120 VLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIOA 179
|||||:|||||:|||||
Db 1094 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIOA 1153

Qy 180 KIPGLKRKAE 189
|||||
Db 1154 KIPGLKRKAE 1163

RESULT 10

Q7YRW9

ID Q7YRW9 PRELIMINARY; PRT; 184 AA.
AC Q7YRW9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RTN4w (Fragment).
GN RTN4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164744; AAP47319.1; -.
FT NON_TER 1 1
SQ SEQUENCE 184 AA; 20671 MW; DE990E03BBAF84A1 CRC64;

Query Match 96.8%; Score 901; DB 6; Length 184;
Best Local Similarity 98.9%; Pred. No. 2.1e-73;
Matches 182; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSD 65

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Db      1 LYWRDIKKTGVVFGXXLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSD 60
Qy      66 EGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVF 125
Db      61 EGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVF 120
Qy      126 TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 185
Db      121 TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 180
Qy      186 RKAE 189
Db      181 RKAE 184

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RESULT 11

Q8K3G7

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ID   Q8K3G7      PRELIMINARY;      PRT;      357 AA.
AC   Q8K3G7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nogo-B.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Jin W., Li R., Long M., Shen J., Ju G.;
RT   "Cloning and expression of the mouse Nogo-B protein.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AY114153; AAM77069.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

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```

Query Match          96.7%; Score 900.5; DB 11; Length 357;
Best Local Similarity 97.9%; Pred. No. 5e-73;
Matches 185; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

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Qy      2 VDDLlyWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 60
Db      169 VDDLlyWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 228
Qy      61 IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
Db      229 IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 288
Qy      121 LMWVFtyVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180

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          |||||||||||||||||||||:|||||||||||||||||:|||||||||
Db      289 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 348

Qy      181 IPGLKRKAE 189
          |||||||
Db      349 IPGLKRKAE 357

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RESULT 12

Q7T224

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ID      Q7T224      PRELIMINARY;      PRT;      199 AA.
AC      Q7T224;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RTN4-C.
GN      RTN4.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22715887; PubMed=12832288;
RA      Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT      "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT      RTN/Nogo gene family.";
RL      FASEB J. 17:1238-1247(2003).
DR      EMBL; AY164737; AAP47312.1; -.
SQ      SEQUENCE      199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;

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Query Match          94.7%; Score 882; DB 13; Length 199;
Best Local Similarity 93.6%; Pred. No. 1.2e-71;
Matches 176; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 61
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 71

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 121
          |||||||||||||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      72 QKSDEGHPFRAYLESDDVAIVEDLIQKYSSVVLGHINGTVKELRRLFLVDDLVDLSLKFAVL 131

Qy      122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLVKNKNVKDAMAKIQAKI 191

Qy      182 PGLKRKAE 189
          ||||| |
Db      192 PGLKRKTE 199

```

RESULT 13

Q9GM33

```

ID      Q9GM33      PRELIMINARY;      PRT;      179 AA.
AC      Q9GM33;

```

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS *Macaca fascicularis* (Crab eating macaque) (*Cynomolgus* monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB049853; BAB16739.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

Query Match 93.1%; Score 867; DB 6; Length 179;
 Best Local Similarity 98.3%; Pred. No. 2.4e-70;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 11 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPF 70
 :|||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVIAIQKSDEGHPF 60
 Qy 71 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGA 130
 |||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLRFVLMWVFTYVGA 120
 Qy 131 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 189
 |||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179

RESULT 14

Q7T222

ID Q7T222 PRELIMINARY; PRT; 214 AA.

AC Q7T222;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4-M.

GN RTN4.

OS *Carassius auratus* (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; *Carassius*.

OX NCBI_TaxID=7957;

RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164754; AAP47329.1; -.
SQ SEQUENCE 214 AA; 24063 MW; E9B603B043159DD9 CRC64;

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Qy	2	VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI	61
Db	27	VVDLLYWRDLQRTGVVFGASLLLLLSVCSIIISVISYVALALLSVTISFRIYKGILQAV	86
Qy	62	QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL	121
Db	87	QKSEDGHPFKMYLDKDIGISSELVQKYSDTALAHINCVIKELRRLFLVEDLVDLSLKFAVF	146
Qy	122	MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI	181
Db	147	MWILTYVGALFNGLTLLIMGLIGTFSWPVIYEKHQAQIDHYGLVNKQIKDVMGKIQAKI	206
Qy	182	PGLKRKAE	189
Db	207	PGAKPKTE	214

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ID   Q9BQ59.          PRELIMINARY;          PRT;       199 AA.
AC   Q9BQ59;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to reticulon 1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003003; AAH03003.1; -.
DR   EMBL; BC000314; AAH00314.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   GO; GO:0000786; C:nucleosome; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IEA.
DR   GO; GO:0006334; P:nucleosome assembly; IEA.
DR   InterPro; IPR001951; Histone_H4.
DR   InterPro; IPR003388; Reticulon.

```

DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE_H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 199 AA; 22642 MW; 7CFA44CC568DF6D8 CRC64;

Query Match 73.3%; Score 682; DB 4; Length 199;
 Best Local Similarity 68.4%; Pred. No. 1.3e-53;
 Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

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Qy      3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 62
      :|||||||:|:|:| | || ||| |:| | |:| | | ||||| |:|:|
Db      13 IDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQ 72

Qy      63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLM 122
      |:|||||:| | | |: |:| :| |:| |:| | | | | | | | | | | | | | | | | |
Db      73 KTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLM 132

Qy      123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
      |: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      133 WLLTYVGALFNGLTLLMAVVSMTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 192

Qy      183 GLKRKAE 189
      | | | |
Db      193 GAKRHAE 199
  
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Search completed: September 29, 2004, 18:19:48
 Job time : 15.8689 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:04:48 ; Search time 2.70944 Seconds
(without alignments)
3632.211 Million cell updates/sec

Title: US-09-830-972-29_COPY_990_1178
Perfect score: 931
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query			ID	Description
Result	No.	Score	Match	Length	DB			
1	931	100.0	1192	1	RTN4_HUMAN		Q9nqc3	homo sapien
2	911	97.9	199	1	RTN4_MOUSE		Q99p72	mus musculu
3	908	97.5	1163	1	RTN4_RAT		Q9jkl1	rattus norv
4	682	73.3	776	1	RTN1_HUMAN		Q16799	homo sapien
5	681	73.1	777	1	RTN1_RAT		Q64548	rattus norv
6	624.5	67.1	236	1	RTN3_HUMAN		O95197	homo sapien
7	623.5	67.0	237	1	RTN3_MOUSE		Q9es97	mus musculu
8	473.5	50.9	545	1	RTN2_HUMAN		O75298	homo sapien
9	473	50.8	471	1	RTN2_MOUSE		O70622	mus musculu
10	93.5	10.0	197	1	AR61_DROME		Q9ves1	drosophila
11	88.5	9.5	1278	1	NPC1_HUMAN		O15118	homo sapien
12	88	9.5	468	1	ACH5_HUMAN		P30532	homo sapien
13	87.5	9.4	296	1	YBZ7_YEAST		P38279	saccharomyc
14	84	9.0	744	1	PRES_RAT		Q9eph0	rattus norv
15	83	8.9	578	1	MDLB_BUCBP		Q89a96	buchnera ap
16	83	8.9	744	1	PRES_MERUN		Q9jkq2	meriones un
17	83	8.9	744	1	PRES_MOUSE		Q99nh7	mus musculu

18	82.5	8.9	570	1	SECD_STRCO	Q53955	streptomyce
19	82	8.8	589	1	Y015_MYCGE	P47261	mycoplasma
20	81.5	8.8	324	1	MRAY_LISIN	Q929y0	listeria in
21	81	8.7	329	1	O5T2_HUMAN	Q8ngg2	homo sapien
22	81	8.7	993	1	NISB_LACLA	P20103	lactococcus
23	80.5	8.6	299	1	Y779_METJA	Q58189	methanococc
24	80.5	8.6	470	1	YMP8_CAEEL	P53993	caenorhabdi
25	80.5	8.6	502	1	OXAA_AQUAE	O66561	aquifex aeo
26	80.5	8.6	839	1	TLR4_PANPA	Q9ttn0	pan paniscu
27	80	8.6	744	1	PRES_HUMAN	P58743	homo sapien
28	79.5	8.5	499	1	UBPG_YEAST	Q02863	saccharomyc
29	79	8.5	312	1	OLF2_CHICK	P37068	gallus gall
30	79	8.5	388	1	YUBA_BACSU	O32086	bacillus su
31	79	8.5	839	1	TLR4_HUMAN	O00206	homo sapien
32	78	8.4	349	1	MRAY_CHLPN	Q9z706	chlamydia p
33	78	8.4	507	1	TLCB_RICPR	Q9zdf2	rickettsia
34	78	8.4	607	1	GLMS_AGRT5	Q8uehl	a glucosami
35	77.5	8.3	267	1	YTXD_BACME	P46826	bacillus me
36	77.5	8.3	503	1	C72R_ARATH	Q9sael	arabidopsis
37	77.5	8.3	1277	1	NPC1_PIG	P56941	sus scrofa
38	77	8.3	580	1	MDLB_BUCAI	P57552	buchnera ap
39	76.5	8.2	221	1	YA78_AQUAE	O67171	aquifex aeo
40	76	8.2	284	1	HTPX_METJA	Q59076	methanococc
41	76	8.2	286	1	YL33_ARCFU	O28147	archaeoglob
42	76	8.2	556	1	NU2M_PODAN	P15578	podospora a
43	76	8.2	4351	1	FAT2_RAT	O88277	rattus norv
44	75.5	8.1	307	1	OXA2_LACPL	Q88wr8	lactobacill
45	75.5	8.1	328	1	YM31_ARCFU	O28052	archaeoglob

ALIGNMENTS

RESULT 1

RTN4_HUMAN

ID RTN4_HUMAN STANDARD; PRT; 1192 AA.

AC Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;

AC Q9Y5U6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)

DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific

DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).

GN RTN4 OR NOGO OR ASY OR KIAA0886.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RX MEDLINE=20129242; PubMed=10667780;

RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,

RA Michalovich D., Simmons D.L., Walsh F.S.;

RT "Inhibitor of neurite outgrowth in humans.";

RL Nature 403:383-384(2000).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=21010696; PubMed=11126360;
 RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
 RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
 RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
 RL Oncogene 19:5736-5746(2000).
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20237542; PubMed=10773680;
 RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
 RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
 RT 2p14-->2p13 by radiation hybrid mapping.";
 RL Cytogenet. Cell Genet. 88:101-102(2000).
 RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 4).
 RA Jin W.-L., Ju G.;
 RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Placenta, and Skeletal muscle;
 RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in human.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [6]

RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fibroblast;
 RA Yutsudo M.;
 RT "Isolation of a cell death-inducing gene.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 RN [7]

RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Pituitary;
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
 RA Luo B., Hu R., Chen J.;
 RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [8]

RP SEQUENCE FROM N.A. (ISOFORM 3).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel human cDNA clone with function of inhibiting cancer cell
 RT growth.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [9]

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=99156230; PubMed=10048485;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 5:355-364(1998).
 RN [10]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=20499367; PubMed=11042152;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
 RT "Cloning and functional analysis of cDNAs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells.";
 RL Genome Res. 10:1546-1560(2000).
 RN [12]
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
 RC TISSUE=Brain;
 RA Mao Y.M., Xie Y., Zheng Z.H.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 RN [13]
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RA Sha J.H., Zhou Z.M., Li J.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [14]
 RP TOPOLOGY.
 RC TISSUE=Brain;
 RX MEDLINE=20129259; PubMed=10667797;
 RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
 RT "Identification of the Nogo inhibitor of axon regeneration as a
 RT Reticulon protein.";
 RL Nature 403:439-444(2000).
 RN [15]
 RP FUNCTION.
 RC TISSUE=Brain;
 RX MEDLINE=21069055; PubMed=11201742;
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;
 RT "Identification of a receptor mediating Nogo-66 inhibition of axonal

RT regeneration.";
 RL Nature 409:341-346(2001).
 RN [16]
 RP REVIEW.
 RX MEDLINE=21888956; PubMed=11891768;
 RA Ng C.E.L., Tang B.L.;
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
 RT regeneration.";
 RL J. Neurosci. Res. 67:559-565(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults.
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
 CC This is likely consecutive to their change in subcellular
 CC location, from the mitochondria to the endoplasmic reticulum,
 CC after binding and sequestration.
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum
 CC through 2 putative transmembrane domains.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
 CC IsoId=Q9NQC3-1; Sequence=Displayed;
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
 CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
 CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
 CC Name=4;
 CC IsoId=Q9NQC3-4; Sequence=VSP_005654;
 CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
 CC widely expressed excepted for the liver. Isoform 3 is expressed in
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
 CC specific.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -!- CAUTION: Ref.11 sequence differs from that shown due to
 CC frameshifts in positions 1149 and 1156.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ251383; CAB99248.1; -.
 DR EMBL; AJ251384; CAB99249.1; -.
 DR EMBL; AJ251385; CAB99250.1; -.
 DR EMBL; AB040462; BAB18927.1; -.
 DR EMBL; AB040463; BAB18928.1; -.
 DR EMBL; AF148537; AAG12176.1; -.
 DR EMBL; AF148538; AAG12177.1; -.
 DR EMBL; AF087901; AAG12205.1; -.
 DR EMBL; AF320999; AAG40878.1; -.
 DR EMBL; AF132047; AAD31021.1; -.
 DR EMBL; AF132048; AAD31022.1; -.

DR EMBL; AB015639; BAA83712.1; -.
 DR EMBL; AF077050; AAD27783.1; -.
 DR EMBL; AF177332; AAG17976.1; -.
 DR EMBL; AB020693; BAA74909.1; -.
 DR EMBL; BC001035; AAH01035.1; -.
 DR EMBL; BC007109; AAH07109.1; -.
 DR EMBL; BC014366; AAH14366.1; -.

Query Match 100.0%; Score 931; DB 1; Length 1192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-71;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60
 |||||
 Db 1004 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1063
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
 |||||
 Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123
 Qy 121 LMWVFTYVGFALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
 |||||
 Db 1124 LMWVFTYVGFALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183
 Qy 181 IPGLKRKAE 189
 |||||
 Db 1184 IPGLKRKAE 1192

RESULT 2

RTN4_MOUSE

ID RTN4_MOUSE STANDARD; PRT; 199 AA.
 AC Q99P72; Q9CTE3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
 GN RTN4 OR NOGO.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3T3-L1; TISSUE=Adipocyte;
 RA Coulson A.C., Craggs P.D., Morris N.J.;
 RT "Mouse vp20/RTN4C cDNA."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 170-199 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults (By
 CC similarity).
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
 CC membrane of the endoplasmic reticulum through 2 putative
 CC transmembrane domains (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms may be produced;
 CC Name=1;
 CC IsoId=Q99P72-1; Sequence=Displayed;
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF326337; AAK08076.1; -.
 DR EMBL; AK003859; -; NOT_ANNOTATED_CDS.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT DOMAIN 1 25 CYTOPLASMIC (Potential).
 FT TRANSMEM 26 50 POTENTIAL.
 FT DOMAIN 51 137 LUMENAL (Potential).
 FT TRANSMEM 138 162 POTENTIAL.
 FT DOMAIN 163 199 CYTOPLASMIC (Potential).

FT DOMAIN 12 199 RETICULON.
SQ SEQUENCE 199 AA; 22466 MW; 07BE5D580059ED9C CRC64;

Query Match 97.9%; Score 911; DB 1; Length 199;
Best Local Similarity 98.4%; Pred. No. 1.4e-70;
Matches 185; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 61
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 71

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKLFAVL 121
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLKLFAVL 131

Qy     122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
        ||||||||||||||||||||||||:||||||||||||||||||:||||||||||
Db     132 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKI 191

Qy     182 PGLKRKAE 189
        |||||||
Db     192 PGLKRKAE 199
```

RESULT 3

RTN4_RAT

ID RTN4_RAT STANDARD; PRT; 1163 AA.
AC Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE (Glut4 vesicle 20 kDa protein).
GN RTN4 OR NOGO.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
RX MEDLINE=99249816; PubMed=10231557;
RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:
RT a new member of the reticulon family."
RL Biochim. Biophys. Acta 1450:68-76(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129258; PubMed=10667796;
RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
RA Spillmann A.A., Christ F., Schwab M.E.;
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
RT antigen for monoclonal antibody IN-1."
RL Nature 403:434-439(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;

RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in rat: one of two
 RT minor splice variants.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=22033691; PubMed=12037567;
 RA GrandPre T., Li S., Strittmatter S.M.;
 RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
 RL Nature 417:547-551(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults (By
 CC similarity).
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
 CC membrane of the endoplasmic reticulum through 2 putative
 CC transmembrane domains (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=Nogo-A, NI-220-250;
 CC IsoId=Q9JK11-1; Sequence=Displayed;
 CC Name=2; Synonyms=Nogo-B, Foocen-M1;
 CC IsoId=Q9JK11-2; Sequence=VSP_005658;
 CC Name=3; Synonyms=Nogo-C, VP20;
 CC IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
 CC Name=4; Synonyms=Foocen-M2;
 CC IsoId=Q9JK11-4; Sequence=VSP_005659;
 CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
 CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
 CC present in dorsal root ganglion, sciatic nerve and PC12 cells
 CC after longer exposure. Isoforms 2 and 3 are detected in kidney,
 CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high
 CC level in skeletal muscle. In adult animals isoform 1 is expressed
 CC mainly in the nervous system.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF051335; AAF01564.1; -.
 DR EMBL; AJ242961; CAB71027.1; -.
 DR EMBL; AJ242962; CAB71028.1; -.
 DR EMBL; AJ242963; CAB71029.1; -.
 DR EMBL; AF132045; AAD31019.1; -.
 DR EMBL; AF132046; AAD31020.1; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.
 DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT DOMAIN 1 989 CYTOPLASMIC (Potential).
 FT TRANSMEM 990 1010 POTENTIAL.
 FT DOMAIN 1011 1104 LUMENAL (Potential).
 FT TRANSMEM 1105 1125 POTENTIAL.
 FT DOMAIN 1126 1163 CYTOPLASMIC (Potential).
 FT DOMAIN 976 1163 RETICULON.
 FT DOMAIN 33 46 POLY-GLU.
 FT DOMAIN 73 76 POLY-ALA.
 FT DOMAIN 140 145 POLY-PRO.
 FT VARSPLIC 1 964 Missing (in isoform 3).
 FT /FTId=VSP_005656.
 FT VARSPLIC 965 975 AVLSAELSKTS -> MDGQKKHWKDK (in isoform
 FT 3).
 FT /FTId=VSP_005657.
 FT VARSPLIC 173 975 Missing (in isoform 2).
 FT /FTId=VSP_005658.
 FT VARSPLIC 192 975 Missing (in isoform 4).
 FT /FTId=VSP_005659.
 FT CONFLICT 1130 1131 MISSING (IN REF. 3; AAD31020).
 SQ SEQUENCE 1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;

Query Match 97.5%; Score 908; DB 1; Length 1163;
 Best Local Similarity 97.4%; Pred. No. 1.6e-69;
 Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
 |||
 Db 975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 1034
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
 |||
 Db 1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1094
 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
 |||:|||||:|||||:|||||
 Db 1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154
 Qy 181 IPGLKRKAE 189
 |||
 Db 1155 IPGLKRKAD 1163

RESULT 4

RTN1_HUMAN

ID RTN1_HUMAN STANDARD; PRT; 776 AA.
 AC Q16799; Q16800; Q16801;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulon 1 (Neuroendocrine-specific protein).
 GN RTN1 OR NSP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).
 RC TISSUE=Lung carcinoma;
 RX MEDLINE=93293865; PubMed=7685762;
 RA Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,
 RA Ramaekers F.C.S., Van de Ven W.J.M.;
 RT "Cloning and expression of alternative transcripts of a novel
 RT neuroendocrine-specific gene and identification of its 135-kDa
 RT translational product.";
 RL J. Biol. Chem. 268:13439-13447(1993).
 RN [2]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=96429995; PubMed=8833145;
 RA Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,
 RA Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;
 RT "Genomic organization of the human NSP gene, prototype of a novel gene
 RT family encoding reticulons.";
 RL Genomics 32:191-199(1996).
 RN [3]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=98228245; PubMed=9560466;
 RA Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,
 RA Roebroek A.J., van de Velde H.J.K., Ramaekers F.C., Broers J.L.;
 RT "Neuronal differentiation is accompanied by NSP-C expression.";
 RL Cell Tissue Res. 292:229-237(1998).
 CC -!- FUNCTION: May be involved in neuroendocrine secretion or in
 CC membrane trafficking in neuroendocrine cells.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=RTN1-A; Synonyms=NSP-A;
 CC IsoId=Q16799-1; Sequence=Displayed;
 CC Name=RTN1-B; Synonyms=NSP-B;
 CC IsoId=Q16799-2; Sequence=VSP_005644;
 CC Name=RTN1-C; Synonyms=NSP-C;
 CC IsoId=Q16799-3; Sequence=VSP_005645, VSP_005646;
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES
 CC AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C
 CC IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.
 CC -!- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; L10333; AAA59950.1; -.
 DR EMBL; L10334; AAA59951.1; -.
 DR EMBL; L10335; AAA59952.1; -.
 DR PIR; A46583; A46583.
 DR PIR; I60904; I60904.
 DR Genew; HGNC:10467; RTN1.

```

DR      MIM; 600865; -.
DR      GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.
DR      GO; GO:0004871; F:signal transducer activity; NAS.
DR      GO; GO:0030182; P:neuron differentiation; TAS.
DR      GO; GO:0007165; P:signal transduction; NAS.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane;
KW      Phosphorylation.
FT      TRANSMEM      603      623      POTENTIAL.
FT      TRANSMEM      726      746      POTENTIAL.
FT      DOMAIN        589      776      RETICULON.
FT      DOMAIN        609      612      POLY-LEU.
FT      VARSPLIC      1      420      Missing (in isoform RTN1-B).
FT                                          /FTId=VSP_005644.
FT      VARSPLIC      1      568      Missing (in isoform RTN1-C).
FT                                          /FTId=VSP_005645.
FT      VARSPLIC      569      588      GPGPLGPGAPPLLFLNKQK -> MQATADSTKMDCVWSNW
FT                                          KSQ (in isoform RTN1-C).
FT                                          /FTId=VSP_005646.
SQ      SEQUENCE      776 AA;  83617 MW;  CA5B6232353096FE CRC64;

Query Match          73.3%;  Score 682;  DB 1;  Length 776;
Best Local Similarity 68.4%;  Pred. No. 1.7e-50;
Matches 128;  Conservative 31;  Mismatches 28;  Indels 0;  Gaps 0;

```

Qy	3	VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ	62
Db	590	IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQ	649
Qy	63	KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLM	122
Db	650	KTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLM	709
Qy	123	WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP	182
Db	710	WLLTYVGALFNGLTLLLMAVVSMTLPVVVYVKHQAQIDQYLGIVRTHINAVVAKIQAKIP	769
Qy	183	GLKRKAE	189
Db	770	GAKRHAE	776

RESULT 5

RTN1 RAT

ID RTN1 RAT STANDARD; PRT; 777 AA.

AC Q64548; Q64547;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Reticulon 1 (Neuroendocrine-specific protein) (S-rex).

GN RTN1 OR NSP.

OS *Rattus norvegicus* (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.

OX NCBI TaxID=10116;

```

RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).
RC STRAIN=Wistar; TISSUE=Brain cortex;
RX MEDLINE=96386034; PubMed=8793864;
RA Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,
RA Georgiev G.P., Buchman V.L.;
RT "Intracellular compartmentalization of two differentially spliced s-
RT rex/NSP mRNAs in neurons.";
RL Mol. Cell. Neurosci. 7:289-303(1996).
CC -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC membrane trafficking in neuroendocrine cells.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=RTN1-B; Synonyms=S-RexB;
CC IsoId=Q64548-1; Sequence=Displayed;
CC Name=RTN1-S; Synonyms=S-RexS;
CC IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
CC PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
CC HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
CC EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
CC TYPES.
CC -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
CC HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
CC DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
CC THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB
CC DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
CC HINDBRAIN.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC -----
DR EMBL; U17604; AAC53046.1; -.
DR EMBL; U17603; AAC53045.1; -.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT TRANSMEM 604 624 POTENTIAL.
FT TRANSMEM 727 747 POTENTIAL.
FT DOMAIN 590 777 RETICULON.
FT DOMAIN 610 613 POLY-LEU.
FT VARSPLIC 1 569 Missing (in isoform RTN1-S).
FT /FTId=VSP_005647.
FT VARSPLIC 570 589 IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW
FT KSQ (in isoform RTN1-S).
FT /FTId=VSP_005648.
SQ SEQUENCE 777 AA; 83001 MW; AF7479C50F28D0AC CRC64;

```

Query Match 73.1%; Score 681; DB 1; Length 777;
 Best Local Similarity 67.9%; Pred. No. 2.1e-50;
 Matches 127; Conservative 32; Mismatches 28; Indels 0; Gaps 0;

```

Qy      3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 62
      :|||||||:|:|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      591 IDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQ 650

Qy      63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAVLM 122
      |:|||||:|||| |: |:| :|||: :|| |:||||||| | | | | | | | | | | |
Db      651 KTDEGHPFKAYLELEITLSQEIQKYTDCLQLYVNSTLKELRRLFLVQDLVDLSLKFAVLM 710

Qy     123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
      |: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     711 WLLTYVGALFNGLTLLMAVVMFTLPVVYVKHQAQVDQYLGLVRTHINTVVAKIQAQIP 770

Qy     183 GLKRKAE 189
      | | | |
Db     771 GAKRHAE 777
  
```

RESULT 6

RTN3_HUMAN

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ID   RTN3_HUMAN      STANDARD;       PRT;   236 AA.
AC   O95197;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like
DE   protein II) (NSPLII).
GN   RTN3 OR NSPL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC   TISSUE=Retina;
RX   MEDLINE=99265974; PubMed=10331947;
RA   Moreira E.F., Jaworski C.J., Rodriguez I.R.;
RT   "Cloning of a novel member of the reticulon gene family (RTN3): gene
RT   structure and chromosomal localization to 11q13.";
RL   Genomics 58:73-81(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Huang X., Zhou Y., Du G., Yuan J., Qiang B.;
RT   "Cloning and expression analysis of a cDNA encoding a novel
RT   neuroendocrine-specific protein-like protein 1: NSPL1.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, Eye, and Lymph;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
  
```

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
 CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL
 CC RETINA.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF059524; AAC99319.1; -.
 DR EMBL; AF059529; AAD20951.1; -.
 DR EMBL; AF059525; AAD20951.1; JOINED.
 DR EMBL; AF059526; AAD20951.1; JOINED.
 DR EMBL; AF059527; AAD20951.1; JOINED.
 DR EMBL; AF059528; AAD20951.1; JOINED.
 DR EMBL; AF119297; AAD26810.1; -.
 DR EMBL; BC000634; AAH00634.1; -.
 DR EMBL; BC010556; AAH10556.1; -.
 DR EMBL; BC011394; AAH11394.1; -.
 DR EMBL; BC022993; AAH22993.1; -.
 DR Genew; HGNC:10469; RTN3.
 DR MIM; 604249; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM 68 88 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT DOMAIN 48 236 RETICULON.
 SQ SEQUENCE 236 AA; 25609 MW; DDC6A4544ABCDFB7 CRC64;

Query Match 67.1%; Score 624.5; DB 1; Length 236;
 Best Local Similarity 60.5%; Pred. No. 3.9e-46;
 Matches 115; Conservative 39; Mismatches 35; Indels 1; Gaps 1;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
 :| ||::|||:|||| ||| :| :|||| ||::|| :|: ||||| ||||| ||||
 Db 47 AVHDLIFWRDVKKTGTFVGGTTLIMLLSLAAFSVISVSYLILALLSVTISFRIYKSVIIQA 106
 Qy 61 IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDSLKFAV 120
 :|||:|||||:||||: :: :| | | |:|: |:| :| : ||||:||||| ||
 Db 107 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAV 166
 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
 ||: ||||:||||:||||| : :||||:||||: ||||:|:| | : ||||
 Db 167 FMWLMTYVGAVFNGITLLILAELLIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQA 226
 Qy 181 IPGL-KRKAE 189
 :||: |:|||
 Db 227 LPGIAKKKAE 236

RESULT 7

RTN3_MOUSE

ID RTN3_MOUSE STANDARD; PRT; 237 AA.
 AC Q9ES97;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Reticulon protein 3.
 GN RTN3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;
 RT "Cloning and expression profile of a novel mouse cDNA encoding a human
 RT RTN3 homolog.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

```

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Potential).
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC -----
DR EMBL; AF195940; AAG31360.1; -.
DR EMBL; BC014697; AAH14697.1; -.
DR MGD; MGI:1339970; Rtn3.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Transmembrane; Endoplasmic reticulum.
FT TRANSMEM 69 89 POTENTIAL.
FT TRANSMEM 167 187 POTENTIAL.
FT DOMAIN 49 237 RETICULON.
SO SEQUENCE 237 AA; 25428 MW; EB60A0A7AC45F0DE CRC64;

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Qy	1	SVVDLLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA	60
		: :: : : : :: : : ::	
Db	48	AVHDLIFWRDVKKTGFEVGTTLIMLLSLAAFSVISVSYLILALLSVTISFRVYKSIVIQA	107
Qy	61	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV	120
		: : : :: : : : : : :	
Db	108	VQKSEEGLPFPKAYLDVDITLSSEAFHNMYMNAAMVHVNKALKLIIRLFVEDLVDSLKLAV	167
Qy	121	LMWVFETYVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAMAKIQAK	180
		: : : : : : : : : :	
Db	168	FMWLMTYVGAVFNGITLLILAELLVFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAQ	227
Qy	181	IPGL-KRKAE	189
		: : :	
Db	228	LPGIAKKKA	237

RESULT 8

```

ID      RTN2_HUMAN      STANDARD;          PRT;    545 AA.
AC      O75298; O60509;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like

```


DE protein 1) (NSPLI).
 GN RTN2 OR NSPL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RC TISSUE=Lung carcinoma;
 RX MEDLINE=98360096; PubMed=9693037;
 RA Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;
 RT "cDNA cloning, genomic organization, and expression of the human RTN2
 RT gene, a member of a gene family encoding reticulons.";
 RL Genomics 51:98-106(1998).
 RN [2]
 RP SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).
 RC TISSUE=Brain;
 RX MEDLINE=98191726; PubMed=9530622;
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
 RT "Molecular cloning of a novel mouse gene with predominant muscle and
 RT neural expression.";
 RL Mamm. Genome 9:274-282(1998).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=RTN2-A;
 CC IsoId=O75298-1; Sequence=Displayed;
 CC Note=Isoform RTN2-C is produced by alternative initiation at
 CC Met-341 of isoform RTN2-A;
 CC Name=RTN2-B;
 CC IsoId=O75298-2; Sequence=VSP_005649;
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced
 CC by alternative initiation at Met-1 and Met-341;
 CC -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL
 CC MUSCLE.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF004222; AAC32542.1; -.
 DR EMBL; AF004223; AAC32543.1; -.
 DR EMBL; AF004224; AAC32544.1; -.
 DR EMBL; AF038540; AAC14910.1; -.
 DR Genew; HGNC:10468; RTN2.
 DR MIM; 603183; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.
 DR GO; GO:0004871; F:signal transducer activity; NAS.
 DR GO; GO:0007165; P:signal transduction; NAS.
 DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;
 KW Alternative initiation.
 FT CHAIN 1 545 RETICULON PROTEIN 2, ISOFORM RTN2-A.
 FT CHAIN 341 545 RETICULON PROTEIN 2, ISOFORM RTN2-C.
 FT INIT_MET 341 341 FOR ISOFORM RTN2-C.
 FT TRANSMEM 368 388 POTENTIAL.
 FT TRANSMEM 463 483 POTENTIAL.
 FT DOMAIN 345 545 RETICULON.
 FT VARSPLIC 272 344 Missing (in isoform RTN2-B).
 FT /FTid=VSP_005649.
 SQ SEQUENCE 545 AA; 59263 MW; 971FD2F909E1E9E6 CRC64;

Query Match 50.9%; Score 473.5; DB 1; Length 545;
 Best Local Similarity 47.3%; Pred. No. 6.3e-33;
 Matches 95; Conservative 37; Mismatches 56; Indels 13; Gaps 1;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
 | |||||:| : :||| : || | ||||| |::|| || || |::| :||:
 Db 345 VADLLYWKDTRTSGVVFTGLMVSLCLLHFSIVSVA AHLALLLLCGTISLRVYRKVLQAV 404
 Qy .62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAVL 121
 : | :||:|||| : : :| : : | : || |||:||||||| |:
 Db 405 HRGDGANPFQAYLDVDLTLTREQTERLSHQITSRVVSAATQLRHFFLVEDLVDLSLKLALL 464
 Qy 122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
 :: |::||:||||||| :| ||::|::| :||||| |::| : ||:||||
 Db 465 FYILTFVGAIFNGLTLLILGVIGLFTIPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKI 524
 Qy 182 PGL-----KRAE 189
 || | |||
 Db 525 PGTGALASAAAVSGSKAKAE 545

RESULT 9

RTN2_MOUSE

ID RTN2_MOUSE STANDARD; PRT; 471 AA.
 AC O70622; O70620;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like protein 1) (NSPLI).
 GN RTN2 OR NSPL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
 RC STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;
 RX MEDLINE=98191726; PubMed=9530622;
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
 RT "Molecular cloning of a novel mouse gene with predominant muscle and
 RT neural expression."
 RL Mamm. Genome 9:274-282(1998).

RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
 CC (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Brain;
 CC IsoId=O70622-1; Sequence=Displayed;
 CC Name=2; Synonyms=Muscle;
 CC IsoId=O70622-2; Sequence=VSP_005650, VSP_005651;
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular
 CC tissues.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF038537; AAC14906.1; -.
 DR EMBL; AF038537; AAC14907.1; -.
 DR EMBL; AF038538; AAC14908.1; -.
 DR EMBL; AF038539; AAC14909.1; -.
 DR EMBL; AF093624; AAD13195.1; -.
 DR EMBL; BC031370; AAH31370.1; -.
 DR MGD; MGI:107612; Rtn2.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT TRANSMEM 295 315 POTENTIAL.
 FT DOMAIN 272 471 RETICULON.

Query Match 50.8%; Score 473; DB 1; Length 471;
Best Local Similarity 47.0%; Pred. No. 6e-33;
Matches 94; Conservative 38; Mismatches 56; Indels 12; Gaps 1;

RESULT 10

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ID AR61_DROME STANDARD; PRT; 197 AA.
AC Q9VES1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE ARL-6 interacting protein-1 homolog.
GN CG10326.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

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RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of *Drosophila melanogaster*.";

RL Science 287:2185-2195(2000).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- SIMILARITY: Belongs to the ARL6ip family.

CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AE003714; AAF55348.1; -.

DR FlyBase; FBgn0038453; CG10326.

KW Transmembrane.

FT TRANSMEM 43 63 POTENTIAL.

FT TRANSMEM 64 84 POTENTIAL.

FT TRANSMEM 129 149 POTENTIAL.

FT TRANSMEM 150 170 POTENTIAL.

SQ SEQUENCE 197 AA; 22233 MW; 7D35ABAD18CE272E CRC64;

Query Match 10.0%; Score 93.5; DB 1; Length 197;

Best Local Similarity 23.9%; Pred. No. 0.45;

Matches 47; Conservative 25; Mismatches 82; Indels 43; Gaps 7;

Qy 5 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR-----IYKGV 57

:| | | | | | | | : :| | :| :| :|

Db 32 VLTWEKQYYAGVVFGVISCLYLVLWYLDLSLITLLSLLGVISILLNYAFPMVSRLIFGGV 91

Qy 58 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLK 117

| : | | : | | | | : | :| |

Db 92 ---NWDGDQEAKFEDVCGQVCAVKGSLVVWY-----EYLFNERKSTVFV--IVMSLG 138

Qy 118 FAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK- 176
: | :||: | | |: || : : | || ||:: |: :
Db 139 LLAMAW----IGAIINNLLMLYLATLLILMWP-----GLQNKDIFKAITQR 180
Qy 177 ----IQAKIPGLKRKAE 189
| || ||| :
Db 181 ASKIINEKIQCGRKLQ 197

RESULT 11

NPC1_HUMAN

ID NPC1_HUMAN STANDARD; PRT; 1278 AA.
AC O15118; Q9P130;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Niemann-Pick C1 protein precursor.
GN NPC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS NPC1.
RX MEDLINE=97362323; PubMed=9211849;
RA Carstea E.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D.,
RA Cummings C., Gu J., Rosenfeld M.A., Pavan W.J., Krizman D.B.,
RA Nagle J., Polymeropoulos M.H., Sturley S.L., Ioannou Y.A.,
RA Higgins M.E., Comly M., Cooney A., Brown A., Kaneski C.R.,
RA Blanchette-Mackie E.J., Dwyer N.K., Neufeld E.B., Chang T.-Y.,
RA Liscum L., Strauss J.F. III, Ohno K., Zeigler M., Carmi R., Sokol J.,
RA Markie D., O'Neill R.R., van Diggelen O.P., Elleder M.,
RA Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A.;
RT "Niemann-Pick C1 disease gene: homology to mediators of cholesterol
RT homeostasis.";
RL Science 277:228-231(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS.
RX MEDLINE=99355599; PubMed=10425213;
RA Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G.,
RA Carstea E.D.;
RT "The genomic organization and polymorphism analysis of the human
RT Niemann-Pick C1 gene.";
RL Biochem. Biophys. Res. Commun. 261:493-498(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21623216; PubMed=11754101;
RA Bauer P., Knoblich R., Bauer C., Finckh U., Hufen A., Kropp J.,
RA Braun S., Kustermann-Kuhn B., Schmidt D., Harzer K., Rolfs A.;
RT "NPC1: Complete genomic sequence, mutation analysis, and
RT characterization of haplotypes.";
RL Hum. Mutat. 19:30-38(2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99128318; PubMed=9927649;
RA Watari H., Blanchette-Mackie E.J., Dwyer N.K., Glick J.M., Patel S.,

RA Neufeld E.B., Brady R.O., Pentchev P.G., Strauss J.F. III;
 RT "Niemann-Pick C1 protein: obligatory roles for N-terminal domains and
 RT lysosomal targeting in cholesterol mobilization.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:805-810(1999).
 RN [5]
 RP VARIANT NPD TRP-992.
 RX MEDLINE=98299797; PubMed=9634529;
 RA Greer W.L., Riddell D.C., Gillan T.L., Girouard G.S., Sparrow S.M.,
 RA Byers D.M., Dobson M.J., Neumann P.E.;
 RT "The Nova Scotia (type D) form of Niemann-Pick disease is caused by a
 RT G3097-->T transversion in NPC1.";
 RL Am. J. Hum. Genet. 63:52-54(1998).
 RN [6]
 RP VARIANTS NPC1 GLN-934; LEU-940; ASN-948; LEU-954; TRP-992; ALA-1007;
 RP THR-1061 AND VAL-1213.
 RX MEDLINE=99452586; PubMed=10521290;
 RA Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C.,
 RA Neumann P.E.;
 RT "Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich
 RT domain.";
 RL Am. J. Hum. Genet. 65:1252-1260(1999).
 RN [7]
 RP VARIANT NPC1 THR-1061.
 RX MEDLINE=99452593; PubMed=10521297;
 RA Millat G., Marçais C., Rafi M.A., Yamamoto T., Morris J.A.,
 RA Pentchev P.G., Ohno K., Wenger D.A., Vanier M.T.;
 RT "Niemann-Pick C1 disease: the I1061T substitution is a frequent mutant
 RT allele in patients of Western European descent and correlates with a
 RT classic juvenile phenotype.";
 RL Am. J. Hum. Genet. 65:1321-1329(1999).
 RN [8]
 RP VARIANTS NPC1, AND VARIANTS ARG-215; VAL-858 AND GLN-1266.
 RX MEDLINE=99408226; PubMed=10480349;
 RA Yamamoto T., Nanba E., Ninomiya H., Higaki K., Taniguchi M., Zhang H.,
 RA Akaboshi S., Watanabe Y., Takeshima T., Inui K., Okada S., Tanaka A.,
 RA Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G.,
 RA Ohno K.;
 RT "NPC1 gene mutations in Japanese patients with Niemann-Pick disease
 RT type C.";
 RL Hum. Genet. 105:10-16(1999).
 RN [9]
 RP VARIANTS NPC1 GLN-958 AND ALA-1007.
 RX MEDLINE=21313111; PubMed=11349231;
 RA Sun X., Marks D.L., Park W.D., Wheatley C.L., Puri V., O'Brien J.F.,
 RA Kraft D.L., Lundquist P.A., Patterson M.C., Pagano R.E., Snow K.;
 RT "Niemann-Pick C variant detection by altered sphingolipid trafficking
 RT and correlation with mutations within a specific domain of NPC1.";
 RL Am. J. Hum. Genet. 68:1361-1372(2001).
 RN [10]
 RP VARIANTS NPC1 ALA-378; MET-950; ARG-992 AND THR-1061.
 RX MEDLINE=21313105; PubMed=11333381;
 RA Millat G., Marçais C., Tomasetto C., Chikh K., Fensom A.H., Harzer K.,
 RA Wenger D.A., Ohno K., Vanier M.T.;
 RT "Niemann-Pick C1 disease: correlations between NPC1 mutations, levels
 RT of NPC1 protein, and phenotypes emphasize the functional significance
 RT of the putative sterol-sensing domain and of the cysteine-rich
 RT luminal loop.";

RL Am. J. Hum. Genet. 68:1373-1385(2001).
 RN [11]
 RP VARIANTS NPC1 TYR-177; CYS-978 AND VAL-1035.
 RX MEDLINE=21372069; PubMed=11479732;
 RA Ribeiro I., Marcao A., Amaral O., Sa Miranda M.C., Vanier M.T.,
 RA Millat G.;
 RT "Niemann-Pick type C disease: NPC1 mutations associated with severe
 RT and mild cellular cholesterol trafficking alterations.";
 RL Hum. Genet. 109:24-32(2001).
 CC -!- FUNCTION: Involved in the intracellular trafficking of
 CC cholesterol. May play a role in vesicular trafficking in glia, a
 CC process that may be crucial for maintaining the structural and
 CC functional integrity of nerve terminals.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Found in late
 CC endosomes and lysosomes.
 CC -!- DOMAIN: A cysteine-rich N-terminal domain and a C-terminal domain
 CC containing a di-leucine motif necessary for lysosomal targeting
 CC are critical for mobilization of cholesterol from lysosomes.
 CC -!- PTM: Glycosylated.
 CC -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease
 CC type C1 (NPC1) [MIM:257220]. NPC1 is an autosomal recessive lipid
 CC storage disorder, which affects particularly the brain, liver and
 CC spleen, and which is characterized by lysosomal accumulation of
 CC low density lipoprotein derived cholesterol. Clinical features
 CC include variable hepatosplenomegaly and severe progressive
 CC neurological dysfunction such as ataxia, dystonia and dementia.
 CC The age of onset can vary from infancy to late adulthood.
 CC -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease
 CC type D (NPD) [MIM:257250]; also known as Niemann-Pick disease
 CC without sphingomyelinase deficiency, or Nova Scotian type. Because
 CC of evidence from biochemical changes, lack of complementation, and
 CC linkage mapping to the same chromosome site, NPD and NPC1 are
 CC considered to be allelic disorders.
 CC -!- SIMILARITY: Belongs to the patched family.
 CC -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
 CC -----
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 CC -----
 DR EMBL; AF002020; AAB63982.1; -.
 DR EMBL; AF157379; AAD48006.1; -.
 DR EMBL; AF157365; AAD48006.1; JOINED.
 DR EMBL; AF157366; AAD48006.1; JOINED.
 DR EMBL; AF157367; AAD48006.1; JOINED.
 DR EMBL; AF157368; AAD48006.1; JOINED.
 DR EMBL; AF157369; AAD48006.1; JOINED.
 DR EMBL; AF157370; AAD48006.1; JOINED.
 DR EMBL; AF157371; AAD48006.1; JOINED.
 DR EMBL; AF157372; AAD48006.1; JOINED.
 DR EMBL; AF157373; AAD48006.1; JOINED.
 DR EMBL; AF157374; AAD48006.1; JOINED.
 DR EMBL; AF157375; AAD48006.1; JOINED.

DR EMBL; AF157376; AAD48006.1; JOINED.
 DR EMBL; AF157377; AAD48006.1; JOINED.
 DR EMBL; AF157378; AAD48006.1; JOINED.
 DR EMBL; AF338230; AAK25791.1; -.
 DR EMBL; AF123046; AAF28875.1; -.
 DR EMBL; AF123045; AAF28875.1; JOINED.
 DR Genew; HGNC:7897; NPC1.
 DR MIM; 607623; -.
 DR MIM; 257220; -.
 DR MIM; 257250; -.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005764; C:lysosome; TAS.
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0005478; F:intracellular transporter activity; TAS.
 DR GO; GO:0015248; F:sterol transporter activity; TAS.
 DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
 DR InterPro; IPR004765; NP_C_type.
 DR InterPro; IPR003392; Patched.
 DR InterPro; IPR000731; SSD_5TM.
 DR Pfam; PF02460; Patched; 1.
 DR TIGRFAMs; TIGR00917; 2A060601; 1.
 DR PROSITE; PS50156; SSD; 1.

KW Signal; Glycoprotein; Transmembrane; Lysosome; Polymorphism;
 KW Disease mutation.

FT	SIGNAL	1	22	POTENTIAL.
FT	CHAIN	23	1278	NIEMANN-PICK C1 PROTEIN.
FT	TRANSMEM	270	290	POTENTIAL.
FT	TRANSMEM	351	371	POTENTIAL.
FT	TRANSMEM	622	642	POTENTIAL.
FT	TRANSMEM	655	675	POTENTIAL.
FT	TRANSMEM	678	698	POTENTIAL.
FT	TRANSMEM	760	780	POTENTIAL.
FT	TRANSMEM	833	853	POTENTIAL.
FT	TRANSMEM	1099	1119	POTENTIAL.
FT	TRANSMEM	1125	1145	POTENTIAL.
FT	TRANSMEM	1196	1216	POTENTIAL.
FT	TRANSMEM	1228	1248	POTENTIAL.
FT	DOMAIN	249	259	POLY-PRO.
FT	DOMAIN	620	785	SSD.
FT	SITE	1275	1278	DI-LEUCINE MOTIF.
FT	CARBOHYD	70	70	N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 9.5%; Score 88.5; DB 1; Length 1278;
 Best Local Similarity 25.7%; Pred. No. 8.1;
 Matches 39; Conservative 25; Mismatches 51; Indels 37; Gaps 7;

Qy	46	SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRR	105
		:: : : : : : : :	
Db	598	NLTISFTAERSIEDELNRESDSVF-----TVVISYAIMFLYISLALGH----IKSCRR	647
Qy	106	LFLVDD-----LVDSLKFAVLMWVFTYVGALFNGLTLLILALI-----SLF	146
		: : : : ::: : :	
Db	648	L-LVDSKVSLGIAGILIVLSSVACSLGVFSYIGL---PLTLIVIEVIPFLVLAVGVDNIF	703
Qy	147	SVPVIYERHQ----AQIDHYLGLANKNVKDAM	174
		: : : :	
Db	704	ILVQAYQORDERLQGETLDQQLGRVLGEVAPSM	735

RESULT 12

ACH5_HUMAN

ID ACH5_HUMAN STANDARD; PRT; 468 AA.
AC P30532; Q15824; Q99554;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-5 chain precursor.
GN CHRNA5 OR NACHRA5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92179225; PubMed=1542648;
RA Chini B., Clementi F., Hukovic N., Sher E.;
RT "Neuronal-type alpha-bungarotoxin receptors and the alpha 5-nicotinic
RT receptor subunit gene are expressed in neuronal and nonneuronal human
RT cell lines.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1572-1576(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
RT beta 4 subunits.";
RL J. Mol. Neurosci. 7:217-228(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97162233; PubMed=9009220;
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
RT expression of seven nAChR subunits in the human neuroblastoma cell
RT line SH-SY5Y and/or IMR-32.";
RL FEBS Lett. 400:309-314(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Duga S., Solda G., Asselta R., Bonati M.T., Dalpra L., Malcovati M.,
RA Tenchini M.L.;
RT "Characterization of the genomic structure of human nicotinic
RT acetylcholine receptor CHRNA5/A3/B4 gene cluster: identification of
RT two novel introns in the 3' untranslated region of CHRNA3 and of a
RT tail-to-tail overlap between CHRNA3 and CHRNA5.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
 CC extensive change in conformation that affects all subunits and
 CC leads to opening of an ion-conducting channel across the plasma
 CC membrane.
 CC -!- SUBUNIT: Neuronal AChR seems to be composed of two different type
 CC of subunits: alpha and non-alpha (betA).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
 CC -----
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 DR EMBL; M83712; AAA58357.1; -.
 DR EMBL; U62434; AAB40112.1; -.
 DR EMBL; Y08419; CAA69696.1; -.
 DR EMBL; AJ306481; CAC34820.1; -.
 DR EMBL; AJ306482; CAC34820.1; JOINED.
 DR EMBL; AJ306483; CAC34820.1; JOINED.
 DR EMBL; AJ306484; CAC34820.1; JOINED.
 DR EMBL; AJ306485; CAC34820.1; JOINED.
 DR EMBL; AJ306486; CAC34820.1; JOINED.
 DR EMBL; BC033639; AAH33639.1; -.
 DR PIR; A38223; A38223.
 DR Genew; HGNC:1959; CHRNA5.
 DR MIM; 118505; -.
 DR InterPro; IPR006029; Neu_channel_memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;

KW Transmembrane; Multigene family.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 468 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-5 CHAIN.
 FT DOMAIN 23 249 EXTRACELLULAR.
 FT TRANSMEM 250 274 POTENTIAL.
 FT TRANSMEM 282 299 POTENTIAL.
 FT TRANSMEM 316 337 POTENTIAL.
 FT DOMAIN 338 429 CYTOPLASMIC.
 FT TRANSMEM 430 448 POTENTIAL.
 FT DISULFID 170 184 BY SIMILARITY.
 FT DISULFID 234 235 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 23 34 RCGLAGAAGGAQ -> ALRSSRARRAAR (IN REF. 1).
 FT CONFLICT 128 128 V -> S (IN REF. 1).
 FT CONFLICT 365 365 C -> S (IN REF. 1).
 FT CONFLICT 398 398 D -> N (IN REF. 2 AND 4).
 FT CONFLICT 405 405 R -> T (IN REF. 1).
 SQ SEQUENCE 468 AA; 53054 MW; 7FE91A2E362289C0 CRC64;

Query Match 9.5%; Score 88; DB 1; Length 468;
 Best Local Similarity 20.9%; Pred. No. 3.2;
 Matches 40; Conservative 29; Mismatches 66; Indels 56; Gaps 5;

Qy 24 LLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPE 70
 \ :|:||||| :| : | : : ||:| : | :| |
 Db 288 VLVSLTVFLLVIEEIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHRSSSTHNA 347
 Qy 71 RAYL-----ESEVAISEELVQKYSNSALGHVNCTIKEL 103
 | | | :| : : :|| : : :
 Db 348 MAPLVRKIFLHTLPKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALDSIRYITRHI 407
 Qy 104 RRLFLVDDLVDLSLKF-----AVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQA 157
 : | :|: || : :| | :| | : : || ||||| :
 Db 408 MKENDVREVVEDWKFIQAQVLDRLMFLWTFLEVS-----IVGSLGLF-VPVIYKWANI 457
 Qy 158 QIDHYLGLANK 168
 | :| |||
 Db 458 LIPVHIGNANK 468

RESULT 13

YBZ7_YEAST

ID YBZ7_YEAST STANDARD; PRT; 296 AA.

AC P38279;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Hypothetical 33.5 kDa protein in MRPS9-YSW1 intergenic region.

GN YBR147W OR YBR1124.

OS *Saccharomyces cerevisiae* (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c;
 RA Entian K.-D., Koetter P., Rose M., Becker J., Grey M., Li Z.,
 RA Niegemann E., Schenk-Groeninger R., Servos J., Wehner E.,
 RA Wolter R., Brendel M., Bauer J., Braun H., Dern K., Duesterhus S.,
 RA Gruenbein R., Hedges D., Kiessau P., Korol S., Krems B., Proft M.,
 RA Siegers K., Baur A., Boles E., Miosga T.,
 RA Schaaff-Gerstenschlaeger I., Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: SOME, TO S.POMBE SPAC2E12.03C AND SPAC17C9.10.
 CC -----
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 CC -----
 DR EMBL; Z36016; CAA85105.1; -.
 DR PIR; S46018; S46018.
 DR GermOnline; 138690; -.
 DR SGD; S0000351; YBR147W.
 DR InterPro; IPR006603; CTNS.
 DR Pfam; PF04193; PQ-loop; 2.
 DR SMART; SM00679; CTNS; 2.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 13 33 POTENTIAL.
 FT TRANSMEM 45 65 POTENTIAL.
 FT TRANSMEM 69 89 POTENTIAL.
 FT TRANSMEM 164 184 POTENTIAL.
 FT TRANSMEM 200 220 POTENTIAL.
 FT TRANSMEM 239 259 POTENTIAL.
 FT TRANSMEM 263 283 POTENTIAL.
 SQ SEQUENCE 296 AA; 33496 MW; 50D65896A1BAFB43 CRC64;

Query Match 9.4%; Score 87.5; DB 1; Length 296;
 Best Local Similarity 27.4%; Pred. No. 2.2;
 Matches 54; Conservative 25; Mismatches 71; Indels 47; Gaps 11;

Qy 17 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY----KGVIQAIQKS-DEGH--- 68
 | || : || :: : || || | : | | :| :| :| |
 Db 61 VMGAMMQNLLP----TMIILAAYYTLADLILLIQCMWYDKEKKSILQEVKKNVDPVHLPP 116
 Qy 69 -----PFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVD-- 115
 | | | || | || : || :|| | | | :|
 Db 117 ANPINETVLQDVFENEYEP LLPRIEEEDS QSYSSLELGR-TIVVKE-RENFNDFLIVSGV 174
 Qy 116 LKFAVLMWVFETYVGFALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMA 175
 | :| | :| || : | : :| || | | :
 Db 175 LIAGILSWYISYCSGLDNGIPKKKPAFEQI-NLP-----AQILGYL-----SAIL 218
 Qy 176 KIQAKIP----GLKRKA 188
 : :|| ||:
 Db 219 YLGS RIPQIVLNFKRKS 235

RESULT 14

PRES_RAT

ID PRES_RAT STANDARD; PRT; 744 AA.
AC Q9EPH0; Q9ERC6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Prestin.
GN SLC26A5 OR PRES.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND TOPOLOGY.
RC TISSUE=Cochlea;
RX MEDLINE=21173705; PubMed=11274441;
RA Ludwig J., Oliver D., Frank G., Kloecker N., Gummer A.W., Fakler B.;
RT "Reciprocal electromechanical properties of rat prestin: The motor
RT molecule of rat outer hair cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4178-4183(2001).
RN [2]
RP SEQUENCE OF 249-668 FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Beisel K.W., Nelson N.C., Beisel C.L., Delimont D.C., He D.Z.Z.,
RA Fritzsche B.;
RT "Dynamic developmental expression of cochlear hair cell genes: prestin
RT and otoferlin.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 1-20 FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Weber T., Zimmermann U., Winter H., Mack A., Koepschall I.,
RA Rohbock K., Zenner H.P., Knipper M.;
RT "Thyroid hormone is a critical determinant for the regulation of the
RT cochlear motor protein prestin.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=20574880; PubMed=11125015;
RA Belyantseva I.A., Adler H.J., Curi R., Frolenkov G.I., Kachar B.;
RT "Expression and localization of prestin and the sugar transporter
RT GLUT-5 during development of electromotility in cochlear outer hair
RT cells.";
RL J. Neurosci. 20:RC116-RC116(2000).
RN [5]
RP MODE OF ACTION, AND MUTAGENESIS OF ASP-154; ASP-155; GLU-169; LYS-177;
RP ARG-197; LYS-233; LYS-235; ARG-236; GLU-277; ARG-281; LYS-283;
RP LYS-285; ASP-332; ASP-342; LYS-409; LYS-557; ARG-558; LYS-559;
RP ARG-571; ARG-572 AND LYS-577.
RX MEDLINE=21317458; PubMed=11423665;
RA Oliver D., He D.Z.Z., Kloecker N., Ludwig J., Schulte U.,
RA Waldegger S., Ruppersberg J.P., Dallos P., Fakler B.;
RT "Intracellular anions as the voltage sensor of prestin, the outer hair
RT cell motor protein.";

RL Science 292:2340-2343(2001).

CC -!- FUNCTION: Motor protein that converts auditory stimuli to length
 CC changes in outer hair cells and mediates sound amplification in
 CC the mammalian hearing organ. Prestin is a bidirectional voltage-
 CC to-force converter, it can operate at microsecond rates. It uses
 CC cytoplasmic anions as extrinsic voltage sensors, probably chloride
 CC and bicarbonate. After binding to a site with millimolar affinity,
 CC these anions are translocated across the membrane in response to
 CC changes in the transmembrane voltage. They move towards the
 CC extracellular surface following hyperpolarization, and towards the
 CC cytoplasmic side in response to depolarization. As a consequence,
 CC this translocation triggers conformational changes in the protein
 CC that ultimately alter its surface area in the plane of the plasma
 CC membrane. The area decreases when the anion is near the
 CC cytoplasmic face of the membrane (short state), and increases when
 CC the ion has crossed the membrane to the outer surface (long
 CC state). So, it acts as an incomplete transporter. It swings anions
 CC across the membrane, but does not allow these anions to dissociate
 CC and escape to the extracellular space. Salicylate, an inhibitor of
 CC outer hair cell motility, acts as competitive antagonist at the
 CC prestin anion-binding site (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein; lateral wall of
 CC outer hair cells.

CC -!- TISSUE SPECIFICITY: Specifically expressed in outer hair cells.
 CC Not detected in other cells of the organ of Corti.

CC -!- DEVELOPMENTAL STAGE: Low levels are present in new-born rats and
 CC up to day 6. Subsequently, levels increase strongly. Adult levels
 CC are detected starting from day 9 in the basal turn of the cochlea,
 CC from day 10-11 in the middle turn, and from day 12 in the apical
 CC turn.

CC -!- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
 CC family.

CC -!- SIMILARITY: Contains 1 STAS domain.

CC -!- DATABASE: NAME=Protein Spotlight;
 CC NOTE=Issue 22 of May 2002;
 CC WWW="<http://www.expasy.org/spotlight/articles/sptlt022.html>".

CC -----

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CC -----

DR EMBL; AJ303372; CAC21555.1; -.
 DR EMBL; AF315652; AAG30297.1; -.
 DR EMBL; AJ428404; CAD21439.1; -.
 DR InterPro; IPR002645; STAS.
 DR InterPro; IPR001902; Sulph_transpt.
 DR Pfam; PF01740; STAS; 1.
 DR Pfam; PF00916; Sulfate_transp; 1.
 DR TIGRFAMs; TIGR00815; sulP; 1.
 DR PROSITE; PS01130; SLC26A; 1.
 DR PROSITE; PS50801; STAS; 1.

KW Motor protein; Cell shape; Transmembrane; Glycoprotein.

FT DOMAIN 1 79 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	80	100	1 (POTENTIAL).
FT	DOMAIN	101	102	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	103	123	2 (POTENTIAL).
FT	DOMAIN	124	131	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	132	152	3 (POTENTIAL).
FT	DOMAIN	153	183	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	184	204	4 (POTENTIAL).
FT	DOMAIN	205	211	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	212	232	5 (POTENTIAL).
FT	DOMAIN	233	253	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	254	274	6 (POTENTIAL).
FT	DOMAIN	275	286	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	287	307	7 (POTENTIAL).
FT	DOMAIN	308	334	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	335	355	8 (POTENTIAL).
FT	DOMAIN	356	374	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	375	395	9 (POTENTIAL).
FT	DOMAIN	396	411	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	412	432	10 (POTENTIAL).
FT	DOMAIN	433	441	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	442	462	11 (POTENTIAL).
FT	DOMAIN	463	479	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	480	500	12 (POTENTIAL).
FT	DOMAIN	501	744	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	525	713	STAS.
FT	CARBOHYD	163	163	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	166	166	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MUTAGEN	154	154	D->N: SHIFTS THE VOLTAGE-SENSITIVITY TO MORE NEGATIVE VALUES.
FT	MUTAGEN	155	155	D->N: SHIFTS THE VOLTAGE-SENSITIVITY TO MORE NEGATIVE VALUES.
FT	MUTAGEN	169	169	E->Q: NO EFFECT.
FT	MUTAGEN	177	177	K->Q: NO EFFECT.
FT	MUTAGEN	197	197	R->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO MORE NEGATIVE VALUES.
FT	MUTAGEN	233	233	K->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO MORE NEGATIVE VALUES; WHEN ASSOCIATED WITH Q-235 AND Q-236.
FT	MUTAGEN	235	235	K->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO MORE NEGATIVE VALUES; WHEN ASSOCIATED WITH Q-233 AND Q-236.
FT	MUTAGEN	236	236	R->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO MORE NEGATIVE VALUES; WHEN ASSOCIATED WITH Q-233 AND Q-235.
FT	MUTAGEN	277	277	E->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO SLIGHTLY MORE POSITIVE VALUES.
FT	MUTAGEN	281	281	R->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-283 AND Q-285.
FT	MUTAGEN	283	283	K->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-218 AND Q-285.
FT	MUTAGEN	285	285	K->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-281-AND Q-283.
FT	MUTAGEN	332	332	D->Q: NO EFFECT.
FT	MUTAGEN	342	342	D->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO MORE POSITIVE VALUES.
FT	MUTAGEN	409	409	K->Q: NO EFFECT.
FT	MUTAGEN	557	557	K->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-

FT				558 AND Q-559.
FT	MUTAGEN	558	558	R->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-
FT				557 AND Q-559.
FT	MUTAGEN	559	559	K->Q: NO EFFECT; WHEN ASSOCIATED WITH Q-
FT				557 AND Q-558.
FT	MUTAGEN	571	571	R->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT				SLIGHTLY MORE POSITIVE VALUES; WHEN
FT				ASSOCIATED WITH Q-572 AND Q-577.
FT	MUTAGEN	572	572	R->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT				SLIGHTLY MORE POSITIVE VALUES; WHEN
FT				ASSOCIATED WITH Q-571 AND Q-577.
FT	MUTAGEN	577	577	K->Q: SHIFTS THE VOLTAGE-SENSITIVITY TO
FT				SLIGHTLY MORE POSITIVE VALUES; WHEN
FT				ASSOCIATED WITH Q-571 AND Q-572.
FT	CONFLICT	251	251	L -> V (IN REF. 2).
FT	CONFLICT	567	567	I -> M (IN REF. 2).
FT	CONFLICT	572	572	R -> S (IN REF. 2).
FT	CONFLICT	612	612	D -> G (IN REF. 2).
FT	CONFLICT	662	663	GI -> VM (IN REF. 2).
SQ	SEQUENCE	744 AA;	81278 MW;	E49E842CF7A3CD58 CRC64;

Query Match 9.0%; Score 84; DB 1; Length 744;
 Best Local Similarity 23.3%; Pred. No. 11;
 Matches 61; Conservative 34; Mismatches 73; Indels 94; Gaps 12;

Qy	3	VDLLYWRDIKKTGVVFGASLFLLLSLTV-----FSIVSVTAYIALAL	44
		: :: : : : : : : : : : : :	
Db	290	IPLEFFAVVMGTGISAGFNLHESYSVDVVGTLPLGLLPANPDTSLFHLVYVDA-IAIAI	348
Qy	45	L--SVTISFR-----IYKGVIAIQKSDEGHPFRAYLESEVAISEELV	85
		: : : : : : : : : : :	
Db	349	VGFSVTISMAKTLANKHGYQVDGNQELIALGICNSI-----GSLFQTFSSIS-CSLSRSLV	402
Qy	86	QKYSNSALGHVNC--TIKELRRLFLVDDLVDLSLKFAVL-----	121
		: : : : : : : : : : : : : :	
Db	403	QEGTGGKTQLAGCLASLMILLVILATGFLFESLPQAVLSAIVIVNLKGMFMQFSDLPFFW	462
Qy	122	-----MWVFTYVGALFNGL-----TLILALISLFSVPVIYERHQAQIDHYLGLANK	168
		: : : : : : : : : : : :	
Db	463	RTSKIELTIWLTTFVSSFLGLDYGLITAVIIALLT-----VIY---RTQSPSYTVLGQL	514
Qy	169	NVKDAMAKIQA-----KIPGLK	185
		: : : : : : : : :	
Db	515	PDTDVYIDIDAYEEVKEIPGIK	536

RESULT 15

MDLB_BUCBP

ID MDLB_BUCBP STANDARD; PRT; 578 AA.

AC Q89A96;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Multidrug resistance-like ATP-binding protein mdlB.

GN MDLB OR BBP424.

OS Buchnera aphidicola (subsp. Baizongia pistaciae).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

: |:|: | || |:|:
Db 175 IALIIMLLYQYFSKPIL 191

Search completed: September 29, 2004, 18:14:47
Job time : 3.70944 secs